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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 27, 2001, 09:00:04 ; Search time 41.13 Seconds (without alignments) 208.911 Million cell updates/sec Run on:

US-09-889-300A-1

614 1 QVQLQQSGAELVRPGTSVKV......ARDGPWFAYWGQGTLVTVSA 116 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

522463 seqs, 74073290 residues

Searched:

Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

/ SIDS2/gcgdata/geneseq/geneseqp/AA1990.DAT:
/ SIDS2/gcgdata/geneseq/geneseqp/AA1990.DAT:
/ SIDS2/gcgdata/geneseq/geneseqp/AA1991.DAT:
/ SIDS2/gcgdata/geneseq/geneseqp/AA1992.DAT:
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/ SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS2/gcgdata/geneseqg/geneseqp/AA1981.DAT:*
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/SIDS2/gcgdata/geneseqg/AA1983.DAT:*
/SIDS2/gcgdata/geneseqg/AA1983.DAT:*
/SIDS2/gcgdata/geneseqg/geneseqp/AA1985.DAT:*
/SIDS2/gcgdata/geneseqg/geneseqp/AA1985.DAT:*
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/SIDS2/gcgdata/geneseqg/AA1985.DAT:*
/SIDS2/gcgdata/geneseqg/geneseqgp/AA1985.DAT:*
/SIDS2/gcgdata/geneseqg/geneseqg/AA1985.DAT:* A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Murine monoclonal	Amino acid sequenc	Mouse C461 Ig heav	Variable region of	Lead binding MAb 1	Heavy chain variab	Mouse MAb 4D12 H c	ME4 Heavy Chain V	MAD ME4 heavy chai	Mouse ME4 heavy ch	Variable heavy cha
SOUTHWANTES			ID		AAW49814	AAR39266	AAW49810	AAW01580	AAR12360	AAR12238	AAR09427	AAW06216	AAW85063	AAW34515
			DB	21	19	14	19	18	12	12	11	18	20	18
			Match Length DB	116	119	138	138	119	137	137	141	141	141	138
	œ	Query	Match	100.0	90.3	90.3	90.3	89.0	83.9	83.9	83.9	83.9	83.9	83.1
			Score	614	554.5	554.5	554.5	546.5	515	515	515	515	515	510.5
		Result	NO.	7	7	m	4	S	9	7	80	6	10	11

Amino acid sequenc	Humanised C4G1 Iq	Fragment of humani	Humanised C4G1 Ig	Amino acid sequenc	Completely humanis	Amino acid sequenc	Sequence encoded b	Anti-hepatitis B h	Mouse-human chimae	Chimeric anti-hepa	Human anti-hepatit	Human anti-hepatit	Human anti-hepatit	Chimeric anti-hepa	Chimeric anti-hepa	Mouse antibody hea	Nematode salivary	Mus musculus antib	Lead binding MAb 1	Variable heavy cha	GMP-140 MAb heavy	Anti-zeta-chain an	Bispecific anti-ze	Molecular pathogen	Murine VH group 1	Murine VH group 1	Murine antibody he	Heavy chain of mon	Anti-idiotype anti	Muring VH group 1	mon	5A8 VH. Synthetic
9 AAW49813 8 AAW07437	4		4	6	4	6	Ø		8 AAW16340							17 AAR88716		9 AAW43913					21 AAY78328						6 AAR74964			3 AAR28806
119 1	222 1	222 1	235 1																				532 2									
20	82.0	N	\sim	$^{\circ}$	\sim	\sim	\vdash	-	\vdash	81.2	81.2	81.2	81.2	81.2	81.2	81.0	80.1	80.1	6.62	79.9	79.4	79.4	79.4	79.3	0.62	78.8	78.7	78.6	78.6	78.5	78.4	78.3
503.5	503.5	503.5	503.5	503.5	503.5	503.5	498.5	498.5	498.5	498.5	498.5	498.5	498.5	498.5	498.5	497.5	492	492	90	490.5	87	487.5	487.5	487	485	484	483	82	482.5	œ		481
12	14	15	16	17	18	1.9	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

Murine; monoclonal antibody; MAK HE2; heavy chain; variable region; human cellular membrane antigen; tumor associated antigen; TAA; Murine monoclonal antibody MAK HE2 variable region heavy chain. AAB10443 standard; protein; 116 AA 12-JAN-2000; 2000WO-EP00174. 99CH-0000051. (first entry) Loibner H; (IGEN-) IGENEON GMBH. vaccine; cancer. WO200041722-A1. 13-JAN-1999; 01-DEC-2000 20-JUL-2000. Eckert H, AAB10443; Mus sp. AAB10443

WPI; 2000-475956/41.

Novel use of antibodies against human cellular membrane antigens for vaccination against cancer

Example 3; Page 47; 54pp; German.

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0;
                                                                     and/or therapeutic vaccination against cancer may be used in low doses (when compared to antibodies against TAA for passive immunotherapy), typically less than 1 mg by injection. The antibodies also have a long continual activity that directly induces immunity and their shelf life is unlimited (fresh vaccination is always possible). This sequence represents the murine monoclonal antibody MAK HEZ variable region heavy chaln fragment which is used in the method of the invention.
                          human cellular membrane antigen, to manufacture a medicament to
prophylactically and/or therapeutically vaccinate against cancer.
The antibodies against tumor associated antigen (TAA) for prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody; inhibition: antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                              This invention describes the novel use of an antibody targeted to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanised immunoglobulin which binds GPIIb/IIIa - derived from
                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the mouse antibody C4G1 mature heavy chain
                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                      Length 116;
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                                                                                                                                                                                                                                   100.0%; Score 614; DB 21;
llarity 100.0%; Pred. No. 2.1e-47;
Conservative 0; Mismatches 0;
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31..35
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW49814 standard; Protein; 119 AA
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92US-0895952.
92US-0944159.
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/note= "
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50..66
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99..108
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nes 116; Conserv
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Matches
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                                                                                chain, used in the method of the invention involving the creation of a humanised in the method of the invention involving the creation of a humanised is capable of binding to CPID/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of detection of GPIID/IIIa antigeng or for isolating platelets.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                       This is the amino acid sequence of the humanised antibody C4G1 heavy
                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIIb; monoclonal antibody; platelet agglutination; humanised antibody.
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mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
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                                                                                                                                                                                                                                                                                                       Score 554.5; DB 19; Length 119; Pred. No. 4.1e-42;
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/label= complementarity_determining_region_1
                                                                                                                                                                                                                                                                                                                                   4; Indels
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/label= signal_peptide
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71abel= light_chain
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                                         5B; 35pp; English.
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                                                                                                                                                                                                                                                                                                       90.3%;
91.6%;
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92US-0895952.
92US-0944159.
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                              119 AA;
                                         Claim 1; Fig
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11-SEP-1992;
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Gaps QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60 20 qvqlqqsgaelvgpgtsvrvsckasgyaftnyliewvkqrpgqglewigviypgsgqtny 79 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116 3; DB 14; Length 138; Indels Score 554.5; DB 14; Pred. No. 4.8e-42; 3; Mismatches 4; 90.3%; 91.6%; Query Match 90.3 Best Local Similarity 91.6 Matches 109; Conservative 80 Q δ Q à

138 AA;

Sequence

AAW49810 standard; Protein; 138 24-SEP-1998 (first entry) AAW49810;

Variable region of mouse antibody C4G1 light chain.

Mouse; antibody C4C1; heavy chain; humanised; immunoglobulin; Ig; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction, unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.

Wus sp

/note= "complementarity determining region" 118 .127
/note= "complementarity determining region" "complementarity determining /note= "mature protein" Location/Qualifiers 20..138 . . 85 /note= Peptide Protein Domain Domain Domain

US5777085-A

07-JUL-1998

93US-0059159. 91US-0812111. 92US-0895952. 92US-0944159. 03-MAY-1993; 20-DEC-1991; 09-JUN-1992; 11-SEP-1992;

95US-0458516

17-MAY-1995;

(PROT-) PROTEIN DESIGN LABS INC.

TSO JY; CO MS,

WPI; 1998-398136/34 N-PSDB; AAV36742 New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.

Disclosure; Fig 2B; 35pp; English.

chain, used in the method of the invention involving the creation of a humanised in the method of the invention involving the creation of a humanised immunoglobulin (19) derived from the mouse C4G1 antibody. The humanised Iq is capable of binding to GPIDL/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transitent ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Iq can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIID/IIIa on their surfaces, for the detection of GPIID/IIIa antigens or for isolating platelets. This is the amino acid sequence of the mouse antibody C4G1 heavy

138 AA; Seguence

2,

Gaps 3 DB 19; Length 138, 90.3%; Score 554.5; DB 1 91.6%; Pred. No. 4.8e-42; 3; Mismatches 109; Conservative Similarity Query Match Best Local Matches

5;

61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116 ò

AAW01580 RESULT

AAW01580;

AAW01580 standard; Protein; 119 AA

(first entry) 22-AUG-1997 Lead binding MAb 14F11 heavy chain variable region.

cosmetic; herbicide; Monoclonal antibody; Fd fragment; lead cation; perfume; pharmaceutical; health care; skin treatment; pesticide;

Mus musculus

WO9639518-A1

12-DEC-1996

96WO-US09258 05-JUN-1996; 95US-0541373 10-OCT-1995; 05-JUN-1995;

(BION-) BIONEBRASKA INC.

Wylie DE; Murray PJ, Lopez 0,

WPI; 1997-043140/04 N-PSDB; AAT58254.

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Horwitz AH,
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N-PSDB; AAQ12018.
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prophylaxis of
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                                                                                                       The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals.
                                                                          The present sequence represents the heavy chain variable region for monoclonal antibody (MAb) 14F11, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells.
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                      61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGP---WFAYWGQGTLVTVSA 116
           for
                     detecting, removing, adding or neutralising heavy metals, such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
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           DNA encoding heavy metal binding polypeptide sequences - used
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                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                               Score 546.5; DB 18;
Pred. No. 2.1e-41;
3; Mismatches 6;
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                                                     Page 63; 125pp; English
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                                                                                                                                                                                                                                                               89.0%;
89.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                    Matches 107; Conservative
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(GREC ) GREEN CROSS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Better MD, Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-178044/24
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ12062
                                                                                                                                                                                                                                119
                               lead cations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9107493-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-1991
                                                     Claim 12;
                                                                                                                                                                                                                                Sèquence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR12360;
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AAR12360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OVOLQOSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 qvhlqqsgaemvrpgtsvkvscrasgyaftnyliewvkqrpgqglewigvinpgsggtty 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human Abs against HIV-1 comprising human ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human antibodies - used in treatment, diagnosis HIV infections.
monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric and comparising heavy and light chains having murine V regions and human c regions. The chimeric MAbs are more effective than murine MAb 4D12 since they have an increased compatibility in humans. The heavy and light chain V regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV See also AAQ12056-61 and AAQ12063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The mouse VH gene product may be used to produce chimeric mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 137;
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Pred. No. 1.5e-38;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 515; DB 12;
Pred. No. 1.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghosh-Dastidar P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse MAb 4D12 H chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR12238 standard; Protein; 137
                                                                                                                                                                                                                                                                                                                                                                                                    83.9%;
84.7%;
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Best Local Similarity 84.7%;
Matches 100; Conservative
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Best Local Similarity 84.77
Matches 100; Conservative
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80 nenfkgkatltadkssstsymqlssltsddsavyfcarghyggyfvmdywgggtsvtvsa 139
                                                                                                                                                                                                                          Chimeric antibody; monoclonal antibody; ME4; antibody engineering; tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma; ovary carcinoma; melanoma; cancer; diagnosis; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The heavy chain variable region (AAW06216) of mouse monoclonal antibody ME4 is the product of a cDNA clone (AAT43441) isolated from a ME4 hybridoma cDNA library. MAD ME4 (19G1) binds to an antigen that is expressed on the surface of human lung, breast, colon and ovary carcinomas and melanomas, but not on most normal adult tissues. The heavy chain and light chain variable regions (see also AAW06215) of ME4 can be linked to human constant regions and expressed in transformed host cells. Novel mouse-human chimeric antibodies (see also AAW06209-14 and AAW06217-18) can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robinson
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                                                                                                                                                                                             region.
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                                                                                     AAW06216 standard; Protein; 141
                                                                                                                                                                                           MAb ME4 heavy chain variable
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88US-0241744.
88US-0243739.
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89US-0382768.
94US-0364001.
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85.0%;
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                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Better MD, Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-011249/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1991;
06-SEP-1988;
08-SEP-1988;
13-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-1988;
                                                                                                                                                        13-FEB-1997
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19-JUN-1989
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                                                                                                                        AAW06216;
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                                                                      AAW06216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murtine) having specificity to an antigen bound by murine monoclonal antibody (MAb) B38.1. The chimeric antibodies can be used for any purpose for which the original murine MAbs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA 116
                                1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYL.IEWVKQRPGQGLEWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                   NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                    genes coding for esp. to 3 tumour
                                                                                                                                                                                                                                                                                                                                                heavy; chain; constant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.9%; Score 515; DB 11; Length 141; 85.0%; Pred. No. 1.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ntibodies - prepd. using murine variable region,
                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; chimera; light; heavy; cl
varlable; antigen; diagnosis; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 123 + Fig 30; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.6e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robinson RR,
                                                                                                                                                                                                                                                                                                          ME4 Heavy Chain V Region (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric mouse-human antibodies constant human region murine va
                                                                                                                                                                                                        AAR09427 standard; Protein; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0241744.
88US-0243739.
88US-0253002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-0367641
89US-0382768
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                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-115825/15
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Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9002569-A.
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21-JUL-1989;
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                                                                                                                                                     Gaps
                                                                                                                                                                                       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
produced that have specificity to human tumour antigens for use in the treatment and diagnosis of human cancer.
                                                                                                                                                                                                            Length 141;
                                                                                                                                                   Indels
                                                                                                                                                10;
                                                                                                              Score 515; DB 18;
Pred. No. 1.6e-38;
4; Mismatches 10;
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us-09-889-300a-1.rag

Variable region coding sequence; constant region epitope; hybridoma; antibody detection; antigen/antibody complex; variable heavy chain.

Mus musculus WO9727486-A1 31-JUL-1997, Ostrow DH;

Hoff JA,

Hackett JR,

Solden AM,

(ABBO) ABBOTT LAB

WPI; 1997-393833/36.

N-PSDB; AAT98832

97WO-US01074. 96US-0589939

17-JAN-1997; 23-JAN-1996;

Variable heavy chain of antibody from hybridoma 5-465-210.

19-MAR-1998 (first entry)

'AAW34515 standard; Protein; 138 AA.

AAW34515

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The present sequence represents the heavy chain variable region of murine antibody ME4. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytocoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the
                                                                                                                      Heavy chain variable region; murine antibody ME4; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric antibody specific for human tumour antigen - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoassay, imaging or antitumour agent
                                                                                              Mouse ME4 heavy chain variable region.
           AAW85063 standard; Protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 30; 92pp; English.
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94US-0364001.
95US-0466034.
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88US-0243739.
88US-0253002.
89US-0367641.
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                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment of human cancer
                                                                                                                                                    treatment; human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Better MD, Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-044574/04.
N-PSDB; AAV71159.
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08-SEP-1988;
13-SEP-1988;
                                                                 16-APR-1999
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                                      AAW85063;
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AAW85063
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                         5;
                                                                                                    61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA 116
                                                                                                                   Gaps
                                                                 1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                          4;
Length 141;
                         10; Indels
Score 515; DB 20;
Pred. No. 1.6e-38;
                         4; Mismatches
83.9%;
85.0%;
 Query Match 83.9
Best Local Similarity 85.0
Matches 102; Conservative
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produced by hybridoma 5-465-10, and can be detected using the method of the invention. The method is for detecting the presence of antibody which the invention. The method is for detecting the presence of antibody which may be present in a test sample. It comprises contacting a test sample cuspected of containing the antibody with an antigen specific for the antibody to allow the formation of antigen/antibody complexes, detecting the presence of the antibody which may be present in the test sample and employing, as a control or calibrator, a reagent which binds to the antigen. The improvement to this method over previous methods, comprises antigen. The improvement region epitopes, where the reagent binds to the antigen can though constant region epitopes, where the reagent binds to the antigen can the also be used for detecting the presence of antibodies developed can be also be used for detecting the presence of antibodies developed can be also be used for detecting the presence of antibodies developed capability more than one antigen. The method is used particularly for the hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all of the problems associated with using an immune sera in the amunifacture of the producibly generated in virtually unlimited quantities and are also useful for quantitating, and monitoring the integrity of, the antigen the produce of the presence of the integrity of, the antigen that the produce of the controls. The present reagents can be readily useful for quantitating, and monitoring the integrity of, the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the variable heavy chain of the antibody
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с
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of antibody constant region epitope(s) - as control or calibrator reagents in assays for detecting the presence of an
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Pred. No. 3.8e-38;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 60; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody in a test sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 83.1
Best Local Similarity 84.9
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 AA;
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chain, used in the method of the invention involving the creation of a humanised immunoglobulin (1g) derived from the mouse C4G1 antibody. The humanised immunoglobulin (1g) derived from the mouse C4G1 antibody. The humanised Ig is capable of binding to GPIDD/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of athrombus, or certain types of cancer cells which develop GPIDJ/IIIa on their surfaces, for the
                                                                                                                                                  Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; scute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                                                   Amino acid sequence of the humanised antibody C4G1 mature heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of the humanised antibody C4G1 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection of GPIIb/IIIa antigens or for isolating platelets.
                                                                                                                                                                                                                                                                                                                                     "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                           "complementarity determining region"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                   AAW49813 standard; Protein; 119 AA
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91US-0812111.
92US-0895952.
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                                                                                     (first entry)
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- Homo sapiens.
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50..66
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AAW49813
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The present sequence is the heavy chain variable region of the group 4b2 putative consensus anti-DNA monoclonal antibody (MAb), which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder.

The sequence was derived by aligning homologous anti-DNA MAb, whose sequences have been published, as well as several MAb of other specificities obtained from a database search.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                                 Heavy chain; variable region; anti-DNA; monoclonal; antibody; 4b2 group; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLE; disease; consensus; putative.
                                                                                                                                                                        Anti-DNA antibody 4b2 group heavy chain variable region.
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/label= framework_III
99..110
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/label= J_region
                                                                                          AAW07437 standard; Protein; 121
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/label= CDR_II
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N-PSDB; AAT43806.
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                                                                                                                                               12-AUG-1997
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Gaps

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Indels

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DB 19; Length 119;

82.0%; Score 503.5; DB 1 80.7%; Pred. No. 1.4e-37; 12; Mismatches

Conservative

Best_Local Similarity Matches 96; Conserv

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Query Match

1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

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RESULT 1

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This is the amino acid sequence of a fragment of humanised antibody C4G1 heavy chain, used in the method of the invention involving the creation of a humanised immunoglobulin (gg) derived from the mouse C4G1 antibody. The humanised Ig is capable of binding to GPIDL/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient isofemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIDL/IIIa on isolating platelets.
                                   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                      Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ignouse C4G1; antibody; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embdeep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
                 1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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80.7%; Pred. No. 2.6e-37;
iive 12; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                       Fragment of humanised antibody C4G1 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 7C; 35pp; English.
                                                                                                                                                                                                                        AAW49817 standard; Protein; 222
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92US-0895952.
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Best Local Similarity 80.7%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Homo sapiens
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09-JUN-1992;
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                                                                                                                                                                                                        61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-----PWFAYWGQGTLVTVS 115
                                                                                                                                                                                                                            Gaps
                                                                                                                                                  1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin, H-chain, platelet membrane glycoprotein, GPIIa/IIIb, monoclonal antibody, platelet agglutination, humanised antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA protein - for treating disorders related to vascular thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the sequence of the humanised C4G1 immunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain Fab fragment. See AAR39268 for the F(ab')2 sequence. The antibody is specific for the platelet membrane glycoprotein GPIIa/IIIb and inhibits platelet agglutination. The Ig is thus useful in the treatment of thrombosis.
                                                                                         5;
                                                    Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%; Score 503.5; DB 14; Length 222; 80.7%; Pred. No. 2.6e-37; 1ve 12; Mismatches 8; Indels 3;
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31..35
/label- complementarity_determining_region_1
                                                                                       13; Indels
                                                      DB 18;
                                                    Score 503.5; DB 1 Pred. No. 1.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised C4G1 Ig heavy-chain Fab fragment.
                                                                                         3; Mismatches
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/label= CDR_2
99..108
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/label- CDR_3
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92US-0895952.
92US-0944159.
                                                    82.0%;
82.5%;
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                                                    Query Match 82.0
Best Local Similarity 82.5
Matches 99; Conservative
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Best Local Similarity
Matches 96; Conserv
121
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3;

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Gaps

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Conservative

Length 222; Indels

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Search completed: December 27, 2001, 09:01:00 Job time: $\bf 56$ sec

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22, Appl
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Sequence 7, Appli
Sequence 10, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 65, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 28, Appli
Sequence 15, Appli
Sequence 14, Appli
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1 QVQLQQSGAELVRPGTSVKV......ARDGPWFAYWGQGTLVTVSA 116
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
4.5
Compugen Ltd
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US-08-589-939-1
US-08-458-516-10
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US-08-458-516-13
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US-08-458-516-13
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US-08-15-12-12
US-08-17-128-20
US-08-17-128-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212252 segs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
GenCore version
Copyright (c) 1993 · 2000
                                                                                                                                                                                                                December 27, 2001, 09:00:04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                       protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                                                                                                                                                                                                                                                                               US-09-889-300A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
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Match 1
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Perfect score:
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116 1 US-08-487-200-14 116 1 US-08-488-113B-167 116 1 US-08-477-484B-167 116 1 US-08-477-484B-167 116 1 US-08-477-788A-85 116 2 US-08-477-531B-53 116 2 US-08-477-531B-53 116 2 US-08-63-360-167 116 4 US-09-136-389-167 116 4 US-09-136-389-167 116 4 US-08-484-537-14 118 4 US-08-484-537-14 118 4 US-07-987-264-14 239 3 US-08-486-11 599 1 US-08-486-11 599 1 US-08-486-11	ALIGNMENTS	S/08458516 g manized Antibodies Reactive IIB/IIIA 3 s. Smith laza, Steuart Tower, Suite elease #1.0, Version #1.25 A: 0S/08/458,516 US/08/458,516 US/08/458,516 US 08/059,159 1193 ION: M. M. MATION: A: 30,223 ER: 11823-37-3 MATION: 30,223 III: S: ids	90.3%; Score 554.5; DB 1; 91.6%; Pred. No. 3.3e-45; vative 3; Mismatches 4;
		1 Application U No. 5777085 AL INFORMATION: LICANT: Co, Man Sun LICANT: To, Man Sun LICANT: To, Man Sun LICANT: To, Man Sun LE OF INVENTION: GP BER OF SEQUENCES: 2 BERSPONDENCE ADDRESS: 2 DDRESSEE: William M TREEF: One Market P ITY: San Francisco TATE: California OUNTRY: USA LIVE STAN FRADABLE FORM: EDIUM TYPE: Floppy OWPUTER: IBM PC COMPUTER: ILLING DATE: ON-MARE: ELENT APPLICATION NUMBER: ILLING DATE: ON-MAY AMPLICATION NUMBER: ILLING DATE: ON-MAY AMPLICATION NUMBER: ELERAN: A15-326-242 ELEFAX: 415-326-242 MATION FOR SEQ ID NO UENCE CHARACTERISTIC ELEFAX: 415-326-242 MATION FOR SEQ ID NO UENCE CHARACTERISTIC ENGTH: 119 amino ac YPE: amino acid OPOCIOSY: linear GMENT TYPE: N-termi	Ξ.
44444444444444444444444444444444444444		GENERAL INCRMATION: APPLICANT: APPLICANT: CO. Man Sun APPLICANT: APPLICANT: TITLE OF INVENTION: GONESEPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESS: ADDRESSE: ADDRESS:	atch Sal
00000000000000000000000000000000000000		RESULT 11 US-08-458-5 Sequence Sequence Patent APPLIC APPLIC APPLIC APPLIC TITLE NUMBER CORRES CORRES STRE COMPUT	Query Ma Best Loc Matches

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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSGYGHWYFDVWGAGTTVTVSS 119
                                                                                                                                         ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
                                         APPLICANT: GOEBEL, PETER TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: UUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.0%; Score 546.5; DB 3; 89.9%; Pred. No. 1.9e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 04-DEC-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/541,373

FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/541,373

FILING DATE: 05-JUN-1995

FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                    PETER JOSEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/08589939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Carter, Charles G. REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FRAGMENT TYPE: 1
; ORIGINAL SOURCE:
US-08-767-128-10
                                                                                                                                                                                                                                                  USA
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APPLICANT:
APPLICANT:
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US-08-589-939-1
                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                 3; Gaps
1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQCLEWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                            APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: Callfornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 554.5; DB 1
Pred. No. 3.9e-45;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY, AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 10, Application US/08767128; Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
                                                                                                                                                                                                                                               Sequence 7, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%;
91.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.37
Best Local Similarity 91.65
Matches 109; Conservative
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Length 119; Indels

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                             REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-458-516-22; Sequence 22, Application US/08458516; Patent No. 5777085; GENERAL INFORMATION:
                                                                                                                                                                                                                                                        30,223
                                                                                                                                                                                                                                                                                                                                                                                              119 amino acids
                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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Pred. No. 5.1e-41;
5; Mismatches 10; Indels 3
                                                                 APPLICANT: OSTCOW, David H.
APPLICANT: Golden, Alan M.
TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND TITLE OF INVENTION: CONTROLS
NUMBER OF SOUTHONES: 70
CORRESPONDENCE ADDRESS:
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Patent No. 5777085
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: TSO, J. Yun
TILE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IITA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
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STREEF: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/589,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNET/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5865.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                    APPLICANT: Hackett, Jr., John R. APPLICANT: Hoff, Jane A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO:
SEGULENCE CHARACTERISTICS:
LENGTH: 138 amino acidi
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Best Local Similarity 84.9
Matches 101; Conservative
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                                                                                                                                                                                                                               CITY: Abbott Park
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; Patent No. 6015662
; GENERAL INFORMATION:
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Gaps
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3
Query Match 82.0%; Score 503.5; DB 1; Length 119; Best Local Similarity 80.7%; Pred. No. 2e-40; Matches 96; Conservative 12; Mismatches 8; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Humanized Antibodies Reactive with TITLE OF INVENTION: GPIIB/IIIA NUMBER OF SEQUENCES: 23 CORRESPONDEMES. 23 ADDRESSE: William M. Smith STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
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US-08-458-516-13
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APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCE: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
STRET: San Francisco
STATE: California
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.0%; Score 503.5; DB 1;
80.7%; Pred. No. 3.9e-40;
tive 12; Mismatches 8;
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
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                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2423
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acids
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REFERENCE/DOCKET NUMBER:
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Best Local Similarity 80.73
Matches 96; Conservative
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; MOLECULE TYPE: protein
US-08-458-516-22
                                                                                                                                                                                                                                                                                                                           single
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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                                                                                                                                                                         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                 61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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82.0%; Score 503.5; DB 1; Length 235; 80.7%; Pred. No. 4.1e-40; ive 12; Mismatches 8; Indels 3
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APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 503.5; DB 1 Pred. No. 8.4e-40;
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APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William N.
REGISTATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08458516
Patent No. 5777085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 13:
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80.7%;
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                                                 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: SOFTWARE: Patent1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 96; Conserve
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        Query Match
Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
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RESULT

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Sequence 65, Application US/08881037
Fatent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Sanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mortison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/443,540 FILING DATE: 18-MAY-1995 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-0CT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REGISTRATION NUMBER: 35,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEPAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                          single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-767-128-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-08-881-037-65
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                                                            GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEIPE, Boris
APPLICANT: STEIPE, Boris
APPLICANT: STEIPE, Boris
TILE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P8341-8072
CURRENT PILING DATE: 1994-09-21
CURRENT PILING DATE: 1997-01-14
EARLIER APPLICATION NUMBER: OGY/65,179
EARLIER FILING DATE: 1997-01-14
EARLIER FILING DATE: 1995-01-15
EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER PILING DATE: 1994-07-15
SOFTWARE: PATENTING DATE: 1994-07-15
SOFTWARE: PATENTING DATE: 1994-07-15
SOFTWARE: PATENTING DATE: 1994-07-15
SOFTWARE: PATENTING DATE: 1994-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYL.IEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NEKFKGKATLTRDKSSSTAYLQLSSLTSEDSAVYYCARGGYYYFDYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSES: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.0%; Score 497.5; DB 4; Length 117; 80.3%; Pred. No. 7.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LEAD BINDING POLYDEPTIDES AND TITLE OF INVENTION: NUCLECTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: PCT/US96/09258
05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
  US-09-157-370-2
; Sequence 2, Application US/09157370A
; Patent No. 6262238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08767128; Patent No. 6111079; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
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FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.0%
Best Local Similarity 80.3%
Matches 94; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus sp. US-09-157-370-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 117
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Gaps
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                                                                                                                                  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGPWFAYWGQGTLVTVSA 116
                                                        .
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Query Match 79.9%; Score 490.5; DB 3; Length 119; Best Local Similarity 78.2%; Pred. No. 3.3e-39; Matches 93; Conservative 10; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08737560A

Patent No. 5928833

GENERAL INFORMATION:
APPLICANT: KIM, Joong-Gon
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: RANG, Chang-Yuil
STREET: KANG, Chang-Yuil
STREET: KWANAR-gu
                                                                                                                                                                                                                                                                                                       Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                       Query Match 79.1%; Score 485.5; DB 3; Best Local Similarity 80.0%; Pred. No. 9.7e-39; Matches 96; Conservative 4; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage COMPUTER: IBM PC/AT
203442110710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: LIME FC/AC ACCOUNTS SYSTEM: MS-DOS SOFTWARE: WORD Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/737,560A FILING DATE: 13-NOV-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-8176
FILING DATE: 08-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Republic of Korea ZIP: 151-057
                                                                                                          65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Republic of Korea ZIP: 135-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                           TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER
                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-881-037-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seoul
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US-08-737-560A-10
                                        TELEPHONE:
                                                                                    TELEX:
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TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                            1 QVQLQQPGAELVKPGASVKLSCKASGYTFSSYWMHWVKQRPGQVLEWIGEINPGNGHTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                  61 NEKFKSKATLIVDKSSSTAYMQLSSLTSEDSAVYYCARSFTTARGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                               1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                            61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                       Length 119;
                                                                                     ; OTHER INFORMATION: 4B4-1-1 heavy chain variable region US-08-737-560A-10
                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                    78.6%; Score 482.5; DB 2; 79.0%; Pred. No. 1.8e-38; iive 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION NUMBER: 07/618,542
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
FILING DATE: NO. 5871732ember 27, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 10 SOUTH WACKER DRIVE CHITY. CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: ROSA, MARCARET D.
APPLICANT: ROSA, JOSEPH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
                                                                                                                                                                                                             Best Local Similarity 79.0
Matches 94; Conservative
                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-07-916-098A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
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                                                                      FEATURE:
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us-09-889-300a-1.rai

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                                                                                                                                             61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD-----GPWFAYWGQGTLVTV 114
                                                                                                                                                                Gaps
                                                                      1 OVOLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                           20 EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVVHWVKONPGQGLEWIGYINPFNDGTKY 79
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 Length 122;
                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
; Score 482; DB 2;
; Pred. No. 2.1e-38;
19; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
TITLE OF INVENTION: METHOD OF TREATMENT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/033,827
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STREE: P.O. D.C.
CITY: Charlotte
STATE: No. 5624659th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SIDLEY, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEPHONE: 919-481-3175
                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08392419
; Patent No. 5624659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
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amino acid
                                    88; Conservative
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Matches 91, Conservative
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 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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US-08-392-419-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                    115 SA 116
                                                                                                                                                                                                                                                       121 SS 122
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                                    Matches
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Method for obtaining modified immunogenicity of murine immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.9%; Score 478.5; DB 1; Length 123; 74.0%; Pred. No. 4.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                             TITLE OF INVENTION: Method for obtaining modified or INVENTION: Immunoglobulins with redutive OF INVENTION: antibody variable domains NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
STREET: 215 Y 15, ATABEY PLAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 27, 2001, 09:03:06
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                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                 Sequence 15, Application US/08497312 Patent No. 5712120 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CU 80/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BOND, LAURENCE B. REGISTRATION NUMBER: 30,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: 30-JUN-1995
PRIOR APPLICATION NUMBER: CU 80/
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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Matches 91; Conserv
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US-08-497-312-15
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                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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US-08-497-312-15
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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                                                                              APPLICANT
                                                                                                                                                                                                                                                           STATE:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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sw model using OM protein - protein search,

Search time 25.84 Seconds (without alignments) 341.960 Million cell updates/sec December 27, 2001, 09:00:04 ou:

US-09-889-300A-1 Title: Perfect score:

QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGTLVTVSA 116 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR_68:* Database

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

		Description	Iq heavy chain V r	neavý cha	neavý cha	Iq heavy chain pre	-6 antibody	Iq heavy chain V r	Iq qamma-2b chain	neavy chain	neavy chain	Iq heavy chain V r	Iq heavy chain V r	yamma chain -	Ig gamma-2a chain	Ig heavy chain V r	Ig heavy chain pre	neavy chain	Iq heavy chain pre	neavy chain	neavy chain pr	neavy chain	Ig heavy chain V r	neavy chain V	Ig heavy chain V r	neavy chain pr	Iq heavy chain v r	neavy chain pr	Iq heavy chain V-D	ibody Fab Jel	
		ID	B30560	290098	S20640	A30577	JC2269	C30562	G2MS11	F29380	C30560	S38565	S21810	238950	S40295	E30562	JL0076	D30562	E29380	A27472	S09216	HVMST7	A54378		PL0231		S19966		9	75	367
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	ALTGNMENTS					
Ig heavy chain V r	G28195	7	120	74.9	460	4 5
heavy chain	S37201	7	118	74.9	460	44
heavy chain	S55542	7	116	75.3	462.5	43
heavy chain	A56700	7	115	75.3	462.5	42
Ig heavy chain pre	E32513	7	138	75.5	463.5	41
heavy chain	F48677	7	123	75.5	463.5	40
heavy chain	S66537	7	131	75.6	464	39
heavy chain	B22769	7	120	75.7	465	38
	S38717	7	118	75.7	465	37
heavy chain	S19969	7	121	75.8	465.5	36
heavy	PL0232	7	112	75.8	465.5	35
B leader/Ig	PC4402	4	287	75.9	466	34
heavy chain	A39276	7	141	75.9	466	33
Ig heavy chain pre	MHMS18	-	139	75.9	466	32
Ig heavy chain V r	S25176	7	117	75.9	466	31
t a comment of the co	A30502	~1	112	75.9	400	30

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mouse mono
                                                                  C;Species: Mus musculus (house mouse)
C;Date: 23.Mar-1989 #sequence_revision 23.Mar-1989 #text_change 23.Jul-1999
C;Accession: B30560
T; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of m
                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Residues: 1-123 <MAT>
A.Cross-references: GB-M24269; NID:g195619; PIDN:AAA38373.1; PID:g195620
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
                                      Ig heavy chain V region (28.4.10A) - mouse (fragment)
                                                                                                                                                                                                                                                                                                        A; Reference number: A30560; MUID:89110062
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-123 <MAT>
                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
B30560
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Gaps 7; Length 123; 7; Indels Query Match 87.2%; Score 535.5; DB 2; Best Local Similarity 87.8%; Pred. No. 1e-41; Matches 108; Conservative 1; Mismatches 7;

2; Dρ οy

61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSSPYDYDGYWYFDVWGAGTTVT 120 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR-----DGPW-FAYWGQGTLVT 113 qq οy

114 VSA 116 121 VSS 123 ò

RESULT S60067

5; Mismatches

Conservative

Matches 102;

g ò Ig heavy chain V region - mouse

85.7%; 85.0%;

Query Match Best Local Similarity

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Cispecies: Mus musculus (house mouse)
Cispecies: 33-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
Cistocession: C30562.
Risikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, J. Immunol. 142, 888 #993, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen A;Reference number: A30562; MUID:89110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kurome, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kamihagi, K.; Yasumoto, M.; Ka
J. Blochem. 115, 608-614, 1994
A;Title: Expression of recombinant mouse/human chimeric antibody specific to human GM
A;Reference number: JC2269; MUID:94334310
                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: JC2269; PC2186
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                               20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWINWVKQRPGGGLEWIGNIYPGSSSTNY 79
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;2-98/Region: V segment
                                                                                                                                Length 135;
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                                                                                                                                                                                               16;
                                                                                                                             Score 491; DB 2;
Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.4%; Score 487.5; DB 2
78.6%; Pred. No. 2.2e-37;
                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
C; Keywords: heterotetramer; immunoglobulin F; 34-117/Domain: immunoglobulin homology <IMM>
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F:107-117/Region: J segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PL7-6 antibody heavy chain - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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82.8%;
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                                                                                                                                                                                               96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JC2269
A; Molecule type: mRNA
A; Residues: 1-117 < KUR>
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Matches 92; Conserv
                                                                                                                                Query Match
Best Local Similarity
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A; Status: preliminary
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C; Species: Mus musculus (house)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C; Accession: S0640; S20644
R: Losman, M.; Fasy, T. M.; Novick, K.E.; Monestier, M.
Submitted to the EMBL Data Library, February 1992
A; Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A; Reference number: S20639
A; Accession: S20640
A; Cross-references: EMBL: X65002; NID: G52600; PIDN: CAA46135.1; PID: G52601; EMBL: X64999; N
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin homology <IMM>
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R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof J. Exp. Med. 161, 805-815, 1985
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela A;Reference number: A30577; MUID:85159423
A;Accession: A30577
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Ig heavy chain precursor V region (MRL10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
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                                                                     A; Reference number: A52979; PDB:1FPT A; Conference number: A52979; PDB:1FPT A; Conferents: annotation; X-ray crystallography, 3.0 angstroms, residues C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin; pyroglutamic acid F;15-98 Domain: immunoglobulin homology <IMM> F;15-98 Domain: immunoglobulin homology <IMM> F;15-04 Domain: immunoglobulin homology <IMM> F;15-04 Domain: pyrrolidone carboxylic acid (Gln) #status predicted F;22-96/Disulfide bonds: #status experimental
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Pred. No. 7.5e-41;
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                                       submitted to the Brookhaven Protein Data Bank, January 1995
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80.0%; Score 491.5; DB 2; 77.3%; Pred. No. 9.6e-38; Live 13; Mismatches 11;

Conservative

Query Match Best Local Similarity Matches 92; Conserv

셤 ò g Superfamily: immunoglobulin V region; immunoglobulin homology

A; Molecule type: mRNA A; Residues: 1-135 <KOF> A; Cross-references: GB:M37621

A; Status: preliminary

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Ainthogon 1907, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 20
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Ig heavy chain V region (35.8.2H) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mar-1989 #sequence_revision 03.Aug-1992 #text_change 23.Jul-1999
C.Accession: C30560
R.Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain precursor V region (A003 40/5G7) - mouse (fragment)
C;Specias: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: F29380
C;Accession: F29380
C;Accession: R-T; Rabat, B-L; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variab
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        A; Introns: 138/1; 236/1; 258/1; 368/1
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Matches 94; Conservative
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91: Conserv
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A; Residues: 1-137 <CHE>
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A,Accession: A26232
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A; Residues: 138-172, 'P',174-189,'FP',193-376,'T',378-474 <TU2>
R; Rsollo, R; Rougeon, F.
Nature 296, 761-763, 1982
A; Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma? A; Reference number: A26233; MUID:82173203
A; Contents: b allele
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J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 31.Mar.1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C.Accession: S25057; A26235; A26233; A53598
R.Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
A.Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific A.Recession: S25057
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A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
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R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
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A;Residues: 138-172, P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
                                                                                        3,
    Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: the sequence was determined from the germline gene R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R. Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regine A;Reference number: A26235; MUID:80081501
A;Contents: MPC 11
        DB 2;
Score 487.5; DB 2
Pred. No. 2.2e-37;
9; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A;Cross-references: GB:J00461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
    79.48;
79.08;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:J00461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-474 <FIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma-2b chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A26235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A02157
                                              Best Local Sim
Matches 94;
        Query Match
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R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again A;Reference number: S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma-2a chain (mAb735) - mouse
C;Species: Was musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Seyvords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid E:1.446/Product: Ig gamma-2a chain #status experimental <MAT> F:1-117/Domain: V-D-J region <VDJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                     QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                             20 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGGGLEWIGWIYPGNVNTKY 79
                                                                                                                                                                                                                                                                                                                            61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD----GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEKFKGKATLIVDISSSTAYMQLSSLISEDSAVYFCARGGKFAMDYWGQGTSVTVSS 117
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                                                                                                     Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin F;1137-201/Domain: immunoglobulin homology <IMM>
                                                                                                                                                              Indels
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                                                                                                  Score 483.5; DB 2;
Pred. No. 6e-37;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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Pred. No. 1.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
C; Keywords: heterotetramer; immunoglobulin F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S38950; MUID: 94128242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                        78.7%;
79.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;231-340/Domain: C2 region <CH2> F;341-446/Domain: C3 region <CH3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                           Conservative
                                                                            Query Match
Best Local Similarity
Lac 95; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :ype: protein
1-246 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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[Species: Mus musculus (house mouse)
[Species: Mus musculus (house mouse)
[Species: Mus musculus (house mouse)
[Species: O'Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
[Stacession: S21810
[Stockermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
[Submitted to the EMBL Data Library, January 1991
[A. Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy changer and the embler of the embler of a rearranged vbJ-region of a mouse Ig mu heavy changerence in preliminary
[A. Reference number: S21810
[A. Reference number: BNBL: X56936; NID: 954163; PIDN: CAA40257.1; PID: 954164
[A. Cross-references: EMBL: X56936; NID: 954163; PIDN: CAA40257.1; PID: 954164
[A. Introns: 15/3
[C. Superfamily: Immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (ASWV1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06.Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38565
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
Submitted to the ENBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s h
A;Reference number: S3856
A;Accession: S3856
A;Accession: S3856
A;Accession: S3856
A;Accession: S3856
C;Accession: S3856
C;Superfaminary
A;Molecula type: mRNA
A;Residues: 1-118 <MON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                            A;Cross-references: GB:M24270; NID:q195615; PIDN:AAA38371.1; PID:q195616 Cs. Superfamilty: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA
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                                                                                                                                                                                                                                               78.8%; Score 484; DB 2; 78.0%; Pred. No. 4.6e-37;
                                                                                                                                                                                                                                                                                                     10; Mismatches
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                         A; Molecule type: mRNA
A; Residues: 1-118 <MAT>
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  preliminary
                                                                                                                                                                                                                                                                                                     92;
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Best Local S:
Matches 92
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Matches
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A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bit Accession: B30562; MUD:89110066
A;Accession: B30562
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Mol. Immunol. 25, 859-865, 1988
A; Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A; Reference number: JL0076; MUID:89096973
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C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Accession: E30562
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96, 144-199, 261-321, 367-425/pisulfide bonds: #status predicted
F;229-5/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                        1 OVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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A; Residues: 1-141 (KAA>
A; Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
A; Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-141/Product: Ig heavy chain #status predicted <MAT>
F; 34-1117/Domain: immunoglobulin homology <IMM>
F; 50-54/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
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                                                                                                                                                                                                                         Length 446;
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A;Residues: 1-119 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                 Score 482.5; DB 2;
Pred. No. 2.5e-36;
7; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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Pred. No. 7.7e-37;
9; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (27.10.2) - mouse (fragment)
                                                                                                                                                                                                                    78.68;
79.58;
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Local Similarity 78.2%;
les 93; Conservative 9
                                                                                                                                                                                                              Query Match 78.61
Best Local Similarity 79.51
Matches 93; Conservative
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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: JL0076
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                                                                                              Length 141;
                                                                                                                                    Indels
                                                                                                                                  15;
                                                                                              2;
                                                                                            Score 481; DB 2
Pred. No. 1e-36;
                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Search completed: December 27, 2001, 09:01:39 Job time: 95 sec
F:69-85/Region: complementarity-determining
F:123-135/Region: J2 segment
F:136-141/Region: C
                                                                                            78.38;
77.68;
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Best Local Similarity
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STANDARD;
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P03980;
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                                                                                                                                                                                                                                                                   .....ARDGPWFAYWGQGTLVTVSA 116
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P06329
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                                          Compugen Ltd.
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                    100059 seqs, 36664827 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV02_MOUSE
HV11_MOUSE
HV12_MOUSE
HV13_MOUSE
HV13_MOUSE
HV50_MOUSE
HV50_MOUSE
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HV40_MOUSE
HV3J_HUMAN
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HV14_MOUSE
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Gapop 10.0 , Gapext 0.5
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RA GILLIAM A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA TUCKER P.W.;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA TUCKER P.W.;
RT delta in an IgD-secreting plasmacytoma.";
RI Proc. Neatl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003006; Ig_MC.
DR SMART; SM00406; IGv. 1.
FT CHAIN 21 138 FRAMEWORK 1.
FT CHAIN 21 49 FRAMEWORK 2.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 118 127 COMPLEMENTRITY-DETERMINING 3.
FT DOMAIN 118 127 COMPLEMENTRITY-DETERMINING 3.
FT DOMAIN 118 128 BY SIMILARITY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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    P01786
P01811
P01811
P01812
P01809
P01799
P01772
P01772
P01802
P01772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
13-UUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                       138 AA.
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HV17_MOUSE
HV41_MOUSE
HV42_MOUSE
HV32_MOUSE
HV39_MOUSE
HV30_MOUSE
HV30_MOUSE
HV36_MOUSE
HV36_MOUSE
HV36_MOUSE
HV36_MOUSE
HV31_MOUSE
HV31_MOUSE
HV31_MOUSE
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MEDLINE=81234548; PubMed=6788376;
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          EMBL; J00493; AAA38128.1; -. PIR; A02028; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00529; AAA38170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR, A02034; MHMS18.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                 Best_Local Similarity 76.9
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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SEQUENCE
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HV07_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
-! AISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
DIFFERENTIATED GENES THATH HYBRIDIZE TO THIS ONE, THE AUTHORS
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
                                                                                                                                                                                     Marshak-Rothstein A.;
"The genetic basis of antibody production: the dominant anti-arsonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 EKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD-----GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VOLQOSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKORPGOGLEWIGVINPGSGGTNYN 61
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              76.8%; Score 471.5; DB 1; Length 120; 76.7%; Pred. No. 1.6e-41; ive 8; Mismatches 15; Indels 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A/J;
MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                       SEGMENT, JH2.

InterPro; JR00208; HVMSG7.

InterPro; JR0003506; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Antiarsonate antibody; Hybridoma.

NON TER 120 120

SEQUENCE 120 AA; 13307 MW; FF04E4Al67B654AF CRC64;
                                                                                                                                                                   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
HV02_MOUSE
TH HV02_MOUSE
TO HV0146,
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 16-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse)
           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 36-65.
                                                                                                                                                          MEDLINE-83131846; PubMed-6186498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin heavy chain
Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92; Conservative
                                                                       Mus musculus (Mouse)
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Best Local Similarity
Matches 92; Conserva
                                                                                                                                          SEQUENCE FROM N.A.
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Dp
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-1- MISCELLANEDUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD----GPW-FAYWGQGTLVTVS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1'QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY 79
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Baltimore D.;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR0047; ig_v.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                          76.5%; Score 469.5; DB 1; Length 140; 76.9%; Pred. No. 3.1e-41; tive 9; Mismatches 14; Indels 5.
                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                      140 140
140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV07_MOUSE STANDARD; PRT; 139 AA. P01751; P01752; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1999 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
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us-09-889-300a-1.rsp

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                                                                                                                                                                                                                                                                                                                                        1;
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"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
cell 24:625-637(1981).
-1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR----DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   1 OVOLOQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                              20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                         COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                        COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                                      75.9%; Score 466; DB 1; Length 139; 74.2%; Pred. No. 7.1e-41;
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                                                                                                                                                                                                                                                                                                                                      16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION S43 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 AA.
                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                   BY SIMILARITY
                                                                                            FRAMEWORK 3.
D SEGMENT.
JH2 SEGMENT.
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D SEGMENT.
JH2 SEGMENT.
       FRAMEWORK 1.
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InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Pfam; PF00047; ig; 1, Ig_V.
SWART: SW00406; Icv: 1.
Immunoglobulin V region; Sign&
                                                                                                                                                                                                                                                                                                                                      89; Conservative
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20
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118
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AA;
                                                                                                                                                                                                                                                                                                                  Similarity
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P01755;
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-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                 Gaps
                                                                                                                                        20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79
                                                                                                                          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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                                                                                                                                                                              61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                              61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains."; Biochemistry 21:5415-5424(1982).
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                                                                     Length 137;
                                                                                                17; Indels
                             15200 MW; ADD5881BF44B8EC9 CRC64;
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                                                                  ; Score 457; DB 1;
; Pred. No. 5.8e-40;
12; Mismatches 17,
                                                                                                                                                                                                                                                                           HV12_MOUSE STANDARD; PRT; 117 AA. 201756.
P01756 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
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 BY SIMILARITY
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGv; I.
Immunoglobulin V region; Glycoprotein.
                                                                    74.48;
                                                                                                Conservative
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 115
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Best Local Similarity
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41 1
137 1
137 AA;
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117 AA;
                                                                                 Similarity
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P01757;
21-JUL-1986 (
21-JUL-1986 (
15-JUL-1999 (
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Best Local 3
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HV13_MOUSE
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HV12_MOUSE
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Best Local Similarity
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P01748;
21-JUL-1986 (
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P06329;
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HV04_MOUSE
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Nucleic Acids Res. 84.4839-484(1980).
-!- MISCELLANDUS: THIS SEDUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
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                                                                                                                                                                                                                                                    -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEFTRAN DIFFER FROW THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.
-I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-BANY CHAIN V REGION MPC 11.
Mus musculus (Mouse)
Mus musculus (Mouse)
Musmalla: Butheria: Rodentia: Sciurognathi; Muridae; Murinae: Musinae: Musinae:
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                 Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dextran and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
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                                                                                                                                                                                                                 rearrangements in heavy chain V-region gene segments.";
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM0406; IGv; 1.
Immunoglobulin v region.
DISULFID
HEAVY CHAIN V REGION J558
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGV: 1.
Immunoglobulin V region.
NON TER 121
SEQUENCE 121 AA; 13135
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                     Mus musculus (Mouse)
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                                                                                  NCBI_TaxID-10090;
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P01745;
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REVISIONS.
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HV01_MOUSE
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"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";

EMBO J. 3:517-523(1984).

PIR, A02037, MHMA15.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_W.

SMART; SM040406; IGv; 1.

Immunoglobulin V region.
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                                                    Gaps
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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  Length 121;
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                                                    Indels
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     DB 1;
74.0%; Score 454.5; DB 1
71.9%; Pred. No. 9.1e-40;
ive 11; Mismatches 18
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 23 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 15.3.
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J SEGMENT.
BY SIMILARITY.
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SEGMENT.
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                                                    87; Conservative
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Similarity
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P06330;
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Best Local Si
Matches 81;
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HV51_MOUSE
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                                                                                                                                                                                                "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-!- MISCELLANBOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDINE-85099340: PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 429; DB 1; Length 117; Pred. No. 3.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12772 MW; C530F829C906F69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION VH558 Al/A4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK 3.
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                                                                                                                        STRAIN-C57BL/6;
MEDLINE-81234548; PubMed-6788376;
                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.9%;
81.6%;
                                                                                                                                                                                                                                                                                                            InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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117
54
68
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50
55
69
11
117
117 AA;
                                                                                                                                                                                                                                                                                                  PIR; A02030; HVMS23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                  Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV52_MOUSE
P06327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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Best Local (
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AC P0632_M
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DT 01-JAN
DT 15-JUL
DE 1G HEA'
CC Manmal
CC Manmal
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RN KBLIN
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RT UNTEAT
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"A V region determinant (idiotope) expressed at high frequency in B
1 imphocytes is encoded by a large set of antibody structural genes.";

EMBO J. 3:517-523(1984).

PIR; A02040; MHMS38.

R interPro: IPR003596; Ig_W.

R interPro: IPR003596; Ig_W.

R Pfam; PF00047; Ig; 1.

R SMART: SM0406; IGv; 1.

T DOMAIN 99 104 D SEGMENT.

T DOMAIN 99 104 D SEGMENT.

T DOMAIN 105 118 J SEGMENT.

T DISULFID 22 96 BY SIMILARITY.

T NON_TER 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                          IG HEAVY CHAIN V REGION VH558 A1/A4.
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                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.5%; Score 427; DB 1; Length 117; 83.7%; Pred. No. 5.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Indels
                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                             12971 MW; 8B0BC138856DFC9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.2%; Score 425; DB 1;
68.6%; Pred. No. 9.2e-37;
live 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                            FRAMEWORK 3
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                                                                                                                           Immunoglobulin V region; Signal. SIGNAL
EMBL; M13787; AAA38499.1; -. PIR; A02029; HVMSA1.
                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82; Conservative
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                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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117
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117 AA;
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FRAMEWORK
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                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                     67.48;
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117
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IG HEAVY CHAIN V REG
Mus musculus (Mouse)
                                                                                                                                                                                                                                                41 1
117 1
117 AA;
                                                                                                         PIR; B02034; HVMS61
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6
                                        Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HV05_MOUSE
P01749;
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DISULFID
NON_TER
SEQUENCE
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HV05_MOUSE
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                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 VQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGRIHPSDSDTNYN 80
          61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW--FAYWGQGTLVTVSA 116
                     Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION 102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.4%; Score 414; DB 1; Length 11
81.2%; Pred. No. 1.2e-35;
ive 7; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740A65DD851FCA8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV09_MOUSE STANDARD; PRT; 117 AA. 101753; P11271; 21-JUL-1986 (Rel. 01, Created) 1-JUL-1999 (Rel. 11, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 EKFKGKATLTADKSSTAYMQLSSLTSDDSAVYFCA 97
                                                                                     117 AA
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MEDLINE-81234548; Pubmed-6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12867 MW;
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Best Local Similarity 81.2*
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                    (Mouse)
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                 Baltimore D.;
                                                                                                                                                    Mus musculus
                                                                                   HV06_MOUSE
P01750;
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HV09_MOUSE
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HV06_MOUSE
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                                                                                              "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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                                                                                                                                                                                                                    -i- MISCELLANBOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
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(Rel. 38, Last annotation update)
AIN V REGION 3 PRECURSOR.
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IG HEAVY CHAIN V REGION 3.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
BY SIMILARITY.
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ö 0; Gaps Ouery Match
66.9%; Score 411; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 2.5e-35;
Matches 78; Conservative 9; Mismatches 11; Indels QQ ολ

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Search completed: December 27, 2001, 09:03:33 Job time: 209 sec

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December 27, 2001, 09:00:04; Search time 38.99 Seconds (without alignments) 435.178 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
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sp_phage:*
sp_plant:*
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Maximum DB seq length: 200000000
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76:
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Perfect score:
Sequence:
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                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9d814 mus musculu	Q991c4 mus musculu	mus	09zlc4 mus musculu	mus	mus	mus	Q9z1c6 mus musculu	Q9j183 mus musculu	Q9d9b8 mus musculu	Q9ul94 homo sapien	Q9j177 mus musculu	Q9j181 mus musculu	Q99131 mus musculu	Q9u192 homo sapien	Q9u195 homo sapien	schis	Q9ul89 homo sapien	homod
SUMMARIES				_		_														
SUMD	ID	Q9D8L4	Q99LC4	Q9QXF(Q9Z1C4	090XE	099L25	09JL75	09Z1C6	Q9JL83	Q9D9B8	29UL94	09JL77	09JL81	099L31	29UL92	29UL95	29GYZ2	29UL89	926560
		11	11	11	11	11	11	11	11	11	11	4	11	11	11	4	4	'n	4	4
	Query Match Length DB	473	463	117	118	117	473	109	117	110	111	119	110	114	468	124	125	119	116	157
оP	Query	85.7	77.7	74.7	74.4	73.9	73.8	73.1	70.9	6.69	68.7	67.7	6.99	66.1	62.9	65.8	65.7	9.59	60.7	59.9
	Score	526.5	477	458.5	457	453.5	453	449	435.5	429	422	415.5	411	406	404.5	404	403.5	402.5	373	367.5
	Result No.	1	7	3	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Q9brvO homo sapien Q9185 mus musculu Q97298 homo sapien Q991A6 mus musculu Q9179 mus musculu Q9179 mus musculu Q9179 homo sapien Q9hcal homo sapien Q9hc3 homo sapien Q9h509 homo sapien Q9h509 homo sapien Q9h273 homo sapien	O900W6 oryctolagus O900W4 oryctolagus O9112H Amus musculu O90117 homo sapien O90118 homo sapien O90172 homo sapien O90172 homo sapien O90170 homo sapien
4 090KA4 09185 11 09JL85 4 091298 11 099KA6 11 099KA6 11 099KA4 1 09153 1 099KA4 1 09153 4 09153 4 09153	6 09NOW6 11 09RIA4 4 09UL71 4 09UL91 4 09UL91 1 099M22 1 099U10 1 099W3 1 099W3 4 09UG9
500 1000 1800 2008 1002 1112 1112 1116 1116 1116	124 434 121 121 118 118 118 121 597 112
00000000000000000000000000000000000000	444444444 0.000000000000000000000000000
369.5 359.5 355.5 328.5 312.5 310.5 309.5 309.5 308.5 302.5	301 299 299 290.5 290 290 289.5 277 277 274.5
0110222222222010 0222222222222222222222	w w w w w w w 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

EMBLrel. 17, Creat. EMBLrel. 17, Last. EMBLrel. 17, Last. EMBLrel. 17, Last. ROTEIN. Zoa; Chordata; Crainais Rodentia; Sci. 0; PubMed=11217851 gawa A.; Shibata K a A.; Nishi K. Ki. 1.A. A., Nishi K. Ki. A. Golobori T. uda H.A. Abburne Gaasterland T., G S., Matsuo Y., Ni. 2., Matsuo Y., Ni. 11, D., Bojunga N., Bult C., Fletche Hill D., Hofmann M., Aon Hill D., Hofmann M., Bult C., Fletche Hill D., Hofmann M., Bult C., Fletche Hill D., Hofmann M., Bult C., Fletche Hill D., Hofmann M., Aon Cotation of a full. F. Schoenbach C., Noshida K., Hass Octation of a full. TO IMMUNOGLOBULIN BABZ5349:1; - 13599; 19.	PRESULT 1 ODDBL4 ODDBL6 ODD	; 473 AA.	Created) Last sequence update) Last annotation update)		Craniata; Vertebrata; Euteleostomi;	Sciurognathi; Muridae; Murinae; Mus.			; Yoshino M., Itoh M., Ishii Y.,		Bono H., Kasukawa T., Saito R.,	r M., Batalov S., Casavant T., issi C., King B., Kochiwa H.,	kaido I., Pesole G., Quackenbush J.,	k., Tomita M., Wagner L., Washio F., no H., Baldarelli R., Barsh G.,	, Carninci P., de Bonaldo M.F.,	r C., Fujita M., Gariboldi M., ., Hume D.A., Kamiya M., Lee N.H.,	J., Mazzarelli J., Mombaerts P.,	rouiguez 1:, sakamoto N., , Seya T., Shibata Y., Storch KF.,	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,	egawa i., nawaji H., noncsuki S.,	<pre>length mouse cDNA collection.";</pre>	re 409:585-590(2001). SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
	01-T 1 09-B4 09-D8-L4 09-D8-L4 01-JUN-2001 (Tr 01-JUN-201 (Tr 01-JUN-2	; PRT;	. 17, . 17, . 17,	ROTEIN.			4	: TISSUE=PANCREAS;	.0;	a A., Fukunishi Y., Kor a M. Nishi K. Kivosay	ki Y., Gojobori T., Bor	dda H.A., Ashburner M., Gaasterland T., Gissi	S., Matsuo Y., Nikaido	raubii F., Suzuki K., J T., Furuno M., Aono H.	ili D., Bojunga N., Car	, Bult C., Fletcher C., Hill D., Hofmann M., Hu	ionni L., Mashima J., N	ly B., Kingwald M., Kodi V., Schoenbach C., Sey	oka K., Wang K.H., Wei	., iOsiitda n., naseyawa	otation of a full-lengt	TO IMMUNOGLOBULIN AND	BAB25349 1	4; 1810060009Rik.	. 51 '6676

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us-09-889-300a-1.rspt

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Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 AA
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                                                                                                                                    InterPro; IPR003306; Ig_MHC.
InterPro; IPR003306; Ig_W.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                   EMBL; AJ225171; CAB65236.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                        117
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                         DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO SEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSYYSYDLFAYWGGGTLVTVSA 139
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG---PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGGGTLVTVSA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
BUNS MUSSAULUS (MOUSE).
ELWARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mussinae; Mussinae; Musinae; Musinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.7%; Score 477; DB 11; Length 463; 77.5%; Pred. No. 2.7e-41; tive 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 526.5; DB 11; Length
84.9%; Pred. No. 2.1e-46;
Live 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO03435; AAH03435.1; ...
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                          FRANKT; SMO0407; 19; 4.
SMART; SMO0409; 1G; 2.
SMART; SMO04007; 1Gc1; 3.
SMART; SMO0406; 1Gv; 1.
PROSITE; PS00290; 1G_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090XF0;
01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA
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                       InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_W-V.
InterPro; IPR003597; Ig_c1
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.99
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
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Matches 93; Conserva
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SEQUENCE FROM N.A.
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099LC4

RESULT Q99LC4

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STRAIN=BALB/C;
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Matis L.M., Ewans M.J.,
Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
--- DOMAIN.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLJEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
101-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                74.7%; Score 458.5; DB 11; Length 117; 73.5%; Pred. No. 4.4e-40; tive 16; Mismatches 14; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.4%; Score 457; DB 11; Length 118; 73.7%; Pred. No. 6.4e-40; rative 13; Mismatches 16; Indels
117 AA; 13060 MW; D816AD0858A47E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;
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PRT;
                                                                                                                                                                                                                                                                                                    EMBL; AF206031; AAF69329.1; -. InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596; Ig_v. Ffam: PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1. SMART; SM0406; IGv; 1.
                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                    109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/C;
 113 TVSA 116
                       140 TVSS 143
                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
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                                                                                Q9JL75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q921C6
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                          RESULT
09JL75
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                       qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                            Clemens A., Rademaekers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGP------WFAYWGQGTLV 112
                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_FaxID=10090;
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                         ch 73.9%; Score 453.5; DB 11; Length 117; 1 Similarity 73.7%; Pred. No. 1.5e-39; 87; Conservative 16; Mismatches 12; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.8%; Score 453; DB 11; Length 473; 71.0%; Pred. No. 8.5e-39; 1ve 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003888: AAH03888.1; -. SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                             117
13000 MW; CDDE2AF84D499734 CRC64;
                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1MMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                       117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel: 17, Last annot SIMILAR TO RIKEN CDNA 1810060009 GENE. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
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                       PRT;
                                                                                                                                                                                                      EMBL: AJ225174; CAB65237.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.0%;
Matches 88; Conservative
                                                                                                                                                                                                                                    FF00047; ig; 1.

SM00406; IGv; 1.
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                           (Mouse)
                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=10090;
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                                                                                           Mus musculus
                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
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Best Local 3
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                                   290XE9;
                    090XE9
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S
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Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acety1-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P., Matis L.M., Evans M.J., "Humanized porcine VCAM-specific monoclonal antibodies with chimeric IGG2/64 constant regions block human leukocyte binding to porcine endothelial cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 ELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNYNEKFKGKAT 69
09JL75;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%; Score 449; DB 11;
76.1%; Pred. No. 3.9e-39;
tive 14; Mismatches 10;
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Query Match Best Local

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DR DR TT TS S

Q9JL83;

Q9JL83

RESULT Q9JL83

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STRAIN-CSTBL/63; TISSUB-TESTIS;

A RAINE-21085660; PubMed=11217851;

A Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rubhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nyanahay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:1700110111, FULL INSERT SEQUENCE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SW00409; IG; 1.
SMART; SM00406; IG; 1.
SMART; SM004010; IG_like; 1.
SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;
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Pred. No. 2.5e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003596; Ig_v.
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82.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                          NCBI_TaxID=10090;
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Q9UL94
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         DDE READ DR RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ELVKPGASVKISCKASGYTFSNSWMNWVKLRPGQGLEWIGRIYPGDGDAYYNGKFKGKAT 61
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR-DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-WYOSIN IMMUNGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                  DB 11; Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 LTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW---FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 110 110 110 110 AM; 84E6F2AD219AF95E CRC64;
                                                                                                                                                             117 117
117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                              70.9%; Score 435.5; DB 11; 70.1%; Pred. No. 1.1e-37; ive 13; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 AA
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Mammalia; Eutheria; Rodentia;
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         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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SMART; SM00406; IGv; 1.
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01-JUN-2001
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STRAIN=BALB/C;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNYNEKFKGKAT 69
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                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                     Eukaryota: Medazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QLVRPGASUKISCKASGYSFTSYWHHWVKQRPGQGLEWIGMIDPSDSETRLNQKFKDKAT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.9%; Score 404.5; DB 11; Length 468; 64.7%; Pred. No. 8.7e-34; Live 19; Mismatches 20; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 406; DB 11; Length 114; 68.1%; Pred. No. 1.2e-34; Live 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003878; AAH03878.1; -. SPROUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810066009 GENE.
                                                               Q9JL81;
01-OCT-2000 (TrEMBLrel. 15, Created)
                                                PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
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Matches 77; Conservative
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tes 77; Conservative
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Best Local S:
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                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
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-:- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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Best Local Similarity 74.1%; Pred. No. 3.4e-35;
Matches 80; Conservative 9; Mismatches 17; Indels
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
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Best Local Similarity
-Loc 79; Conservē
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Query Match 65.8%; Score 404; DB 4; Length 124; Best Local Similarity 60.0%; Pred. No. 2.1e-34; Matches 75; Conservative 22; Mismatches 18; Indels 1

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Search time 14.63 Seconds
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268.157 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                               100059 seqs, 36664827 residues
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                                                                                                                                                    December 27, 2001, 09:03:33
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KV5A_MOUSE
KV1A_MOUSE
KV4A_HUMAN
KV4C_HUMAN
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KV1Y_HUMAN
KV1O_HUMAN
KV1V_HUMAN
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KV3J_MOUSE
KV1X_HUMAN
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KV3L_HUMAN
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KV3L_MOUSE
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KV3E_HUMAN
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KV1P_HUMAN
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KV1S_HUMAN
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KV3H_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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	ALIGNMENT PRT; 136 uence upda	PC 21 PRECURSOR. ; Craniata; Vertebrata; Euteleostomi; ; Sciurognathi; Muridae; Murinae; Mu	SEQUENCE FROM N.A. MEDLINE-82059477; PubMed-6170937; MEDLINE-84., Gall M.J., Milstein C.; "Complete sequence of an immunoglobulin nand the dideoxynucleotide method of RNA shulelic Acids Res. 9:4485-4494(1981).	=4638343; sequence of a mc 1972)	This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no war modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).	I_TERM. IG KAPPA CHAIN V-V IG KAPEMEWORK 1. COMPLEMENTARITY-DE FRAMEWORK 2. COMPLEMENTARITY-DE FRAMEWORK 3. COMPLEMENTARITY-DE FRAMEWORK 4. FRAMEWORK 4.
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5.55 61.1 4.45 60.9 4.42 60.9 4.42 60.9 4.41 60.9	USE ST. 1986 (Rel. 1999 (Rel. 1999)	A CHAIN V- culus (Mous ta; Metazos a; Eutheria xID=10090;	E FROM N.A =82059477; P.H., Gait te sequence dideoxynuc	SEQUENCE OF 30-136. MEDLINE=73053310. P. SVASLI J., Milstein "The COMPLETE ANIBO Biochem. J. 128:427	TSS-PROT en the Swiss opean Bioin non-profid and this srequires an email	EMBL; V00810; CAA24192.1 PIR; A01917; KVMS21. InterPro; IPR003006; Ig- InterPro; IPR003596; Ig- Pfam; PF00047; ig; 1. SMART; SM0406; IGV; 1. SIGNAL 1 29 CHAIN 30 136 DOMAIN 53 63 DOMAIN 64 78 DOMAIN 64 78 DOMAIN 118 126 DOMAIN 118 126 DOMAIN 118 126 DOMAIN 118 126 DOMAIN 127 136 NON TER 136 A3; 14990
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0; Gaps
                           30 NIVMTQSPKSMSMSWGERVTLTCKASENVYTVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
                                                                                                                                                                                                                                                                           [2]
SOURDINGE OF 41-149 FROM N.A.
MEDLINE-80176554; PubMed-6245773;
Rabbitts T.H., Hamlyn P.H., Matthyssens G., Roe B.A.;
"The variability, arrangement, and rearrangement of immunoglobulin
                   1 NIVMTQSPKSMSWGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                              Sequence of the full-length immunoglobulin kappa-chain of mouse
                                                                                                                                                                                                                                      Kelley D.E., Colectough C., Perry R.P.;
"Functional significance and evolutionary development of the
5'-terminal regions of immunoglobulin variable-region genes.";
Cell '29:681-689(1982).
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
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Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-V REGION MPC11 PRECURSOR.
0; Mismatches
                                                                                                                                                                                                                                                                                                                           genes.";
Can. J. Biochem. 58:176-187(1980).
                                                                                                                                                                                                                      SEQUENCE OF 1-71 FROM N.A.
MEDLINE-83001944; PubMed-6288267;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 30-149.
MEDLINE-78186617; PubMed-418775;
Matches 107; Conservative
                                                                                                                     STANDARD;
                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                   KV5A_MOUSE
P01633;
                                                                                                                                                                                                                                                                                                                                                                     Smith G.P.;
                                                                                                            KV5A_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                   Length 149;
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149
16434 MW; B0480C87B682AC3E CRC64;
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                                                                                                                                   Score 422; DB 1;
Pred. No. 1.3e-38;
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15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION S107A.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U29423; AAC00033.1; -. PIR; A01915; KYMS7A. HSSP; P01789; 2MCP. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfan; PF00047; Iq; I. SMART; SM00406; IGv; I. Immunoglobulin V region.
                                                                                                                                   75.18;
78.58;
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114 AA;
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Best Local Similarity
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P01632;
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Nucleic Acids Res. 13:6531-6544(1985)
                                       SEQUENCE FROM N.A.
MEDLINE-86041854; Pubmed-2997713;
Marsh P., Mills F., Gould H.;
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MEDLINE≖77038198; PubMed=824717;
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                                                                                                                                                                                                                          EMBL; X02990; CAA26733.1; -. PIR; A01905; K4HU17. HSSP, P01789; 2MCP. InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596; Ig_V.
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  Eukaryota; Metazoa;
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            Mammalia; Eutheria;
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115
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134
134
AA;
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Best Local Similarity
                     NCBI_TaxID=9606;
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ID KV1M_HUMAN
AC P01605;
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                                                                                                                                                                                                                                                                        Salomon A.;
Submitted (AUG-1996) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
1 DIVMTQSPTFLAVTASKKVTISCTASESLYSSKHKVHYLAWYQKKPEQSPKLLIYGASNR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NIVMTQSPKSMSWGERVTLTCKASENVV-----TYVSWYQQKPEQSPKLLIYGASNR 54
                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                Schneider M., Hilschmann N.; "The primary structure of a monoclonic immunoglobulin-L-chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                             55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subgroup IV of the kappa type (Bence-Jones protein Len.).";
Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.1%; Score 383; DB 1; Length 114; 65.5%; Pred. No. 1.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING 1.
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COMPLEMENTARITY-DETERMINING 2.
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01-ARP-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 AAPPA CHAIN V-IV REGION BI7 PRECURSOR.
HOmo sapiens (Human).
                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-IV REGION LEN.
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InterPro; IPR003596; Ig_V.
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P01625;
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P06314;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                          Detection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG KAPPA CHAIN V-IV REGION B17. FRAMEWORK 1.
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                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
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62.8%; Pred. No. 1e-33;
Live 21; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION LAY.
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InterPro; IPR003006; Ig_MHC.
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                                                                                Scand. J. Immunol. 5:677-684(1976).

-!- MISCELLANBOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM VIII KAPPA CHAIN, WITH WHICH IT SHARES CHAIN IDOTYPIC DETERMINANTS.

-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

PIR; A01871; KHULY.

HSSP; P01607; IRE...

InterPro; IPR003006; Ig_MC.

InterPro; IPR003006; Ig_V.

SMART; SM00405; Ig_V.

Immunoglobulin V region.
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                     "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95086080; Pubmed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
Biochemistry 33:14848-14857(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization and preliminary crystallographic data on the VL-telated fragment to of the human KI Bence Jones protein Wat.";
J. Mol. Biol. 147:185-193(1981).
--- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 108;
                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK 1.

34 COMPLEMENTARITY-DETERMINING
49 FRAMEWORK 2.
56 COMPLEMENTARITY-DETERMINING
88 FRAMEWORK 3.
97 COMPLEMENTARITY-DETERMINING
107 FRAMEWORK 4.
88 BY SIMILARITY.
108

A; 11834 MW; 739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 375; DB 1; Length 10
65.4%; Pred. No. 1e-33;
iive 18; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-I REGION WAT.
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MEDLINE-81267384; PubMed-6167731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 65.4 nes 70; Conservative
      Capra J.D., Klapper D.G.;
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108
108 AA;
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P80362;
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SEQUENCE
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KV1Y_HUMAN
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Matches
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"The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bance-Jones protein Rei.); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-76039968; PubMed-1182131;
Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein REI refined at 2.0-A resolution.";
Blochemistry 14:4444-495(1975).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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DOMAIN 24 34 COMMOI PARTIMENT.
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                                                                         Immunoglobulin V region; Bence-Jones protein; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 108
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                                                                                                                                                                                                                                                                                                                                                  11737 MW; D9D941B3F0FAE697 CRC64;
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PIR; A01873; K1HURE.
PDB; 1REI; 17-FEB-84.
                                                                                                                                                                                                                                                                                                                                                                                                                       65.8%; Score 370; DB 1; I 63.6%; Pred. No. 3.5e-33; ative 20; Mismatches 19;
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TN -> SD (IN REF.
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(Rel. 38, Last annotation update)
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
InterPro; IPR003596; 19-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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P01607;
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FRAMEWORK 4.
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MEDLINE=86041853; Pubmed=2997712;
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PIR; A01904; K4HUJI.
HSSP; P01789; ZMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV: 1.
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108 AA;
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Best Local Similarity
Matches 72; Conserv
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P06313;
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SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dwilet F.E., O'Connor T.P., Benson M.D.;
"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73.78(1986).
PIR; A01878; K1HUBN.
HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0030596; Ig_V.
Pfam; PPF0047; ig; 1.
SWART; SM00406; IGV: 1.
Immunoglobulin V region; Amyloid.
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                  COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.9%; Score 365; DB 1; Length 108
63.2%; Pred. No. 1.2e-32;
ive 19; Mismatches 20; Indels
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COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11902 MW; 9E8143E1188BCE2A CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-I REGION BAN.
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P04430:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                    Length 108;
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                                                                                 64.6%; Score 363; DB 1; Length 10
63.6%; Pred. No. 2e-32;
ive 17; Mismatches 22; Indels
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COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                    61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                     61 NFTGSGSGTDFILLTISSLQPEDFATYYCQQYNSYPYTFGGGTKVQIK 107
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11840 MW; CD3FD944FE96FD37 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-ADL-1999 (Rel. 38, Last annotation update)
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Nucleic Acids Res. 13:6515-6529(1985).
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RESULT 11 KV1H_HUMAN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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63.1%;
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
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Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             111 AA;
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                          NCBI_TaxID=10090;
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P04432;
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-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                 Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                             1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                 1 NIVMTQSPKSMSMSVGERVTLTCKASENVV-----TYVSWYQQKPEQSPKLLIYGASNR
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                                                                              55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.9%; Score 359; DB 1;
ilarity 61.7%; Pred. No. 5.4e-32;
Conservative 22; Mismatches 19
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 KAPPA CHAIN VI REGION HAU.
                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01868; KIHUHU.
HSSP; P80362; IWTL.
INCEPERO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; Il_v.
Immarr; SP000406; IGv; I.
Immunoglobulin V region; Bence-Jones protein.
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MEDLINE-71032830; PubMed-4097974;
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hes 66; Conserv
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P01662;
                                                                                                                                                        KV1H_HUMAN
P01600;
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Matches 66;
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SEQUENCE (ABPC 22).
MEDLINE=79012520; PubMed=99744;
McKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      SEQUENCE (PC 9245).
MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaltan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                          Nature 276:785-790(1978).
-i- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL
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COMPLEMENTARITY-DETERMINING 1.
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Pred. No. 5.5e-32;
7; Mismatches 20;
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13-AUG-1987 (Rel. 05, Last sequence update)
13-UL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-I REGION DAUDI PRECURSOR.
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57 GVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
   98
23
108
108 AA;
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                                                                                                                                                                                                                                                                      Mus musculus
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   DOMAIN
DISULFID
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KV3H_MOUSE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The primary structure of the Bence-Jones protein Kue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";
HOPPE-Seyler's Z. Physiol. Chem. 36 10,725-734 (1979).
-I. MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-I. MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
HSP: P01607: IREI.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                  1 NIVMTQSPKSMSMSVGERVTLICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                     23 DIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKPGKAPTLLIYAVSNLQVGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                               IG KAPPA CHAIN V-I REGION DAUDI
                                                                                                                                            FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
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COMPLEMENTARITY-DETERMINING 3.
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                                                                                                                                                                                                                                                              Length 129;
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                                                                                                                                                                                                                                                                                                                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                  14235 MW; CAF076BC7E5574C8 CRC64;
                                                                                                                                                                                                                                                           ; Score 359; DB 1;
; Pred. No. 6.6e-32;
19; Mismatches 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                           108 AA
                                                                                                                                                                                                           BY SIMILARITY.
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                                   EMBL; X00966; CAA24478.1; ALT_TERM. PIR; A01884; K1HUDI. HSSP: PB0362; JWTL. INTERPO; IPR003006; Ig_MHC. INTERPO; IPR003596; Ig_V. Ffan; PP00047; ig; 1. SWART; SW00406; IGV; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=79237924; PubMed=112021;
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IG KAPPA CHAIN V-I REGION KUE.
                                                                                                                                                                                                                                                            63.9%;
59.8%;
                                                                                                                                                                                                                                                                                64; Conservative
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SMART; SM00406; IGV
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Best Local Similarity
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15-JUL-1999 (Rel
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P01604;
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                                                                                                                                                                                                Gaps
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEGUENCE (PC 3741).
MEDLINE-9907315.2; Pubmed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING 1.
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61.3%; Pred. No. 7.1e-32;
ive 21; Mismatches 18; Indels
                                                                                                                                         21; Indels
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                                                                                                                                                                                                                                                   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                      12127 MW; 906679A5D90E4E98 CRC64;
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                                                                                                    63.7%; Score 358; DB 1;
61.7%; Pred. No. 6.9e-32;
tive 20; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                            KV3H_MOUSE STANDARD; PRT; 111 AA. P01660; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 1G KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
FRAMEWORK 4.
BY SIMILARITY.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMAXT; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                         66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 276:785-790(1978).
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Fri Dec 28 08:20:29 2001

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Search completed: December 27, 2001, 09:03:33 Job time: 209 sec

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Q91174 mus musculu Q9U177 homo sapien Q9U177 homo sapien Q9U185 homo sapien Q9U185 homo sapien Q9U179 homo sapien Q9U170 homo sapien Q9U181 homo sapien Q9U186 homo sapien Q9U186 homo sapien Q9U188 musculu Q9T155 mus musculu Q9T155 mus musculu Q9T162 mus musculu Q9T182 mus musculu
                                                             December 27, 2001, 09:02:31 ; Search time 38.99 Seconds (without alignments) 401.414 Million cell updates/sec
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1 NIVWTQSPKSMSNSVGERVT......CGQGYSYPYTFGGGTKLEIK 107
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Copyright (c) 1993 - 2000 Compugen Ltd.
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	ALIGNMENTS PRT; 99 AA. eated) st sequence update; st sequence update; st ennotation updat HT CHAIN VARIABLE F Craniata; Vertebrat Sciurognathi; Murici from mice with aut ELIVE monoclonal ar from mice with aut ELIVEORDAN ABUSH ELIN AND MAJOR HISTE	Score 378; DB 11; Pred. No. 1.1e-33; !; Mismatches 17; VSWYQQKPEQSPKLLIYGAE :
09JLB0 09JLB0 09JLS2 099M11 09ET13 09FT13 09IB02 09IB02 09IB02 09IB05 09IB05 09IB05 09IB05 09IB05 09IB05 09IB05 09IB05 09IB05 09IB05 09IB05 09IB05 09IB06 0 09IB06	PRT; Created) Last seq Last sed Last se	Score 3 Pred. N 8; Mism YVSWYQQK 1:
111	X; 15, 15, 115, ULIN L Ordata dentia dentia dentia 30.1; 39.MW;	38; 78; NVVT : SVSN
103 973 100 100 100 100 100 100 100 100 100 10	AINARY; Blrel. 15, Cz Blrel. 15, Le Blrel. 15, Le Blrel. 15, Le CGCOBULIN II CS COCORTIA CONTRIBUTE CONTRI	67.3%; Conservative SVGERVTLTCKASENVV 1
88888888888888888888888888888888888888	PRELIMIN (TIEMBLr (TIEMBLr (TIEMBLr (TEMBLr IMMUNGGLSS) S (Mouse) Actacos; 10090; 1009	Llarity Conser /GERVTI : :
306 249.5 289.5 221.28 190.5 110.5 111.1 111.23 111.7 111.5 111.3 111.5	DULT L74 G99L74 G99L74 G99L74 O1-OCT-2000 (TrEMBLE-1 15, Creat on the correct on the correc	w O
01000000000000000000000000000000000000	RESULT 11D DT	Query M Best Lo Matches Qy 9

Op Qy

09u410 schistosoma 09n0w5 oryctolagus 09u180 homo sapien 09j178 mus musculu 09j184 mus musculu

58.9 58.9 58.6 58.6 55.7 55.7 55.7 55.0

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Gaps

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Length 109;

us-09-889-300a-2.rspt

RESULT Q9UL77

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2 IVMTQSPKSMSMSVGERVTLTCKASENV-VTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                  65.2%; Score 366.5; DB 4; Length 65.4%; Pred. No. 2.3e-32; Live 20; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                    61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                      109 109
109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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InterPro; IPR003006; Ig_MHC.
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InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
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SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
NON TER 107 107
SEQUENCE 107 AA; 11784
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Best Local Simi
Matches 70;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                       'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.7%; Score 369; DB 4; Length 10
63.6%; Pred. No. 1.2e-32;
Live 20; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C06681716C4D16F3 CRC64;
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                                                                           108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF035037; AAD56273.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA; 11738 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.68
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                            NCBI_TaxID=9606;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             fetus.";
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Q9UL78;
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Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

"Cloning and sequencing of the light chain fragment of variable region genes of an anti-hrnk-a monoclonal antibody.";

J. Cell. Mol. Immunol. 12:21-26(1996).

J. Cell. Mol. Immunol. 2:21-26(1996).

Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

Ti A chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MTQSPKSMSMSVGERVTLTCKASENVV-----TYVSWYQQKPEQSPKLLIYGASNRYTG 57
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.1%; Score 366; DB 11; Length 1
64.5%; Pred. No. 2.5e-32;
tive 17; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;
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RESULT 09UL78

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NON_TER
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SEQUENCE
                                                                                                          Q9UL79;
Q9UL79;
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                                                            01-MAY-2000 (TremBirel. 13, Last sequence update)
01-JUN-2001 (TremBirel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN (PROTEIN FOR MGC:5947).

Was musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Mus.
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                         'Myosin-reactive autoantibodies in rheumatic carditis and normal
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64.7%; Score 363.5; DB 11; Length 238;
Best Local Similarity 59.8%; Pred. No. 1.3e-31;
Matches 67; Conservative 22; Mismatches 18; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 109;
                                                                                                                                                                              Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FSGSGSGTEFTLTISSLQSEDFAIXHCQQYNSWPPIJFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FTGSGSATDFTLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JAS): AAH02035.1; -.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                   11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                64.7%; Score 363.5; DB 4;
65.4%; Pred. No. 4.8e-32;
tive 19; Mismatches 17;
                        109 AA.
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                                            01-MAY 2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last seq) 01-JUN-2001 (TrEMBLrel. 17, Last anno
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                        PRT;
                                                                                                                                                                     MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                 EMBL, AP035029; AAD56265.1; -. HSSP; P01607; 1REI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_M.
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 65.4%
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                 Pfam: PF00047; ig; 1. SMART: SM0406; IGv; 1. NON_TER 1 1 1 1 NON_TER 109 AA: 11761
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                              Homo sapiens (Human)
                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         DOMAIN.
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                                                                                                                                                                                                                       fetus.";
                     Q9UL85;
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RESULT
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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                            20 DVVWTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                   56 TGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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                                                                                                                                                                                                                                                                                           108
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                                                                                                                                                                                                                                                                                                                                          01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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MEDLINE=98277139; PubMed=9614934;
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MEDLINE-98277139; PubMed=9614934;
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108 AA;
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Best Local Similarity
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fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
MYGSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.7%; Score 347; DB 4; Length 108;
61.3%; Pred. No. 2.9e-30;
tive 22; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FSGSGSGTEFTLTISSLQFEDFAVYCQHYNNWPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 FTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                     108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035031; AAD56267.1; HSSP; P01607; 1REI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V. Pfam; PF00047; Ig; 1. SMART; SM0406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035028; AAD56264.1; -. HSSP; P01789; IMCP.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                       Eukaryota; metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.7%
Best Local Similarity 61.3%
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
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Q9UL86;
                                                    Q9UL83,
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Q9UL86
                  RESULT 10
Q9UL83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fetus.";
Clin. Immunopathol. 87:184-192(1998),
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NIVMTQSPKSMSWSGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                      Length 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%; Score 351.5; DB 4; Length Best Local Similarity 61.7%; Pred. No. 9.5e-31; Matches 66; Conservative 20; Mismatches 20; Indels
                                                                                                                                                                                                                                                                    63.0%; Score 354; DB 4; Length 10
63.6%; Pred. No. 5.1e-31;
tive 16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                    108 108
108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF035033, AAD56269.1; --
HSSP, P80362, 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
                                                                  EMBL; AF035044; AAD56280.1; -. HSSP; P01607; 1REI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 AA; 11501 MW;
                                                                                                                                                                                                                                                                                                         68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                         Pfam; PF00047; ig; 1. SMART; SM0406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                     DOMAIN
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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RESULT Q9UL81

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Gaps

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Euteleostomi;

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EMBL; AB036341; BAA88633.1; -.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR0030596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART: SM00406; IGv; 1.
NON TER 1 11
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.0
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C;
                                                                                                                                                                                                            method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09JL82
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Q9JL82
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                                                                                                                                                                                                                                                                                                                                                                        Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                            60.4%; Score 339.5; DB 4; Length 109; 60.7%; Pred. No. 1.9e-29; ive 22; Mismatches 19; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.1%; Score 338; DB 11; Length 214; 58.9%; Pred. No. 6.5e-29; tive 21; Mismatches 23; Indels (
                                                                                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                               109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                               01.MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 AA.
                                                                                                                                                                                                                                            2.14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090YF0;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 2.
SMART; SMO0406; IGv; 1.
SMART; SMO0410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF152371; AAD40242.1; -... HSSP; P01789; 1MCP.
InterPro; IPR003600; Ig_like.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Conservative
                                                                                                  65; Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
                                                                                                                                                                                                                                                                                                           musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA;
                                                                            Ouery Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                     NON_TER
NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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Q9R1A5
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ID 09
AC 09
DT 01
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/Genbank/DDBJ databases:
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody recognizing a cell polarity using a phage display subtraction mathod ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRUB-SPLEEN;
STRAIN=BALBAC, TISSUB-SPLEEN;
Shinohara N., Fowlda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.9%; Score 331; DB 11; Length 298; 57.0%; Pred. No. 5.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BARB/C; TISSUE-SPLEEN;
Shinohara N., Demur T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR033596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 2.
SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CN 8 SCFV.
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5DA8BBFD5F0AA1AE CRC64;

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SONG X.T., Feng Z.O., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
"Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistcsona japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TREMBLRel. 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMEN')
Schistosoma japonicum (Blood fluke).
Eukaryote; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosoma.
NCBI_TAXID=6182;
                                                                                   Gaps
                                                                                                                                      10 SMSMSVGERVTLTCKASENVV----TYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTG 64
                                                                                 5,
                                              58.6%; Score 329.5; DB 11; Length 104; 60.2%; Pred. No. 2.2e-28; ive 18; Mismatches 18; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.5%; Score 328.5; DB 5; Length 106; 61.0%; Pred. No. 2.9e-28; tive 16; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
11478 MW; F20F544426BAE63E CRC64;
                                                                                                                                                                                      65 SGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                      106 AA
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF207620; AAF19434.1; --
HSSP; P01679; 2PBJ.
InterPro; IPPR003006; Ig_MHC.
InterPro; IPPR003596; Ig_v.
Pfam; PF00047; Ig. 1.
SMART; SM00406; IGv; 1.
104 AA; 11360 MW;
                                                                 Local Similarity 60.2
mes 62; Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE 106 AA;
                                                 Query Match
Best Local S:
Matches 62
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 SEQUENCE
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Q9U410
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SCSCSCTSYSLTISRMEAEDAATYYCQQWTSYPFTFGSGTKLELK 106 63 TGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107 g ò QQ

3 VMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRF 62

Best Local Similarity 61.0% Matches 64; Conservative

1;

Gaps

1;

Search completed: December 27, 2001, 09:02:32 Job time: 148 sec

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December 27, 2001, 09:01:00 ; Search time 41.13 Seconds (without alignments) 192.702 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Murine AF2 antibod Variable light cha Scv antibed Scv antibody 24-31 hum Antibody 24-31 hum Variable light sub Antibody 24-31 hum Nariable light sub Antibody 24-31 hum Human Sed antibody Human Eu antibody Murine G250 antibod Anti-idiotype anti FB5 antibody light Protein Sequence o Murine monoclonal	tight lobulin nti-HM1 V regi Single fusion single fusion single
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ALIGNMENTS

AAW47086 standard; Protein; 107 AA

AAW47086

RESULT

Mouse; monoclonal antibody; J591; prostate specific membrane antigen; cancer; vascular endothelial cell; metastatic adenocarcinoma. Mouse J591 monoclonal antibody light chain variable region 97US-0838682. 97WO-US12035 26-JUN-1998 (first entry) WO9803873-A1. 17-JUL-1997; 09-APR-1997; 48-JUL-1996; 29-JAN-1998 AAW47086; Mus sp.

(CORR) CORNELL RES FOUND INC WPI; 1998-120937/11 N-PSDB; AAV13952 Bander NH;

Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for

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present invertible region from an example of the present invention of the present invention describes the elimination of cancer cells by treating vascular endothelial cells (VEC) close to the cancer with an agent (A) able to bind to the extracellular domain (ECD) of prostate specific membrane antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the detection of cancer tissue by detecting binding of labelled (A) to VEC close to, or within, a cancer tissue; (2) eliminating or detecting normal, benignly hyperplastic or ancercus prostate epithelial cells using optionally labelled (A); (3) hybridomas that produce a monoclonal antibody (MAD) that binds to PSMA. The method is used to treat renal, urothelial, colon, lung, rectal or breast cancers and metastatic adenocarcinoma of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cancer (presence of PSMA in the serum indicates that prostate cells are being lysed). (A) binds after cell lysis), allowing targeting of live, unfixed cells and thus providing more efficient treatment and diagnosis. Concert, but normal VEC do not.
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                                                            The present sequence represents the mouse J591 monoclonal antibody light
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                              Example 12; Page 60; 94pp; English.
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Matches 107;
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diagnosis
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This sequence is a fragment of the light chain of the monoclonal antibody 50. The invention relates to an isolated antibody or its antigen binding portion (I) which binds to an extracellular domain of prostate opecific membrane antigen and which does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells. (I) is useful for diagnosis of diseases associated with the presence of normal, benign hyperplastic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when hyperplastic, and cancerous epithelial cells or portions. Also it can be achieved is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used alone or bound to a substance effective to kill cancerous prostate epithelial cells as a therapy for prostate cancer. Binding and internalising of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cytotoxic agents. (I) targets only prostate epithelial cells and other tissue are capital provides safer treatment particularly for elderly patients. The antibodies bind to living prostate cells and treatments using these antibodies are more effective than those which target lysed prostate
            by specific for extracellular prostate-specific membrane antigen, for diagnosis and treatment of prostate cancer \,
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100.0%; Pred. No. 1.2e-39;
                                                                          Example 12; Column 22; 33pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                       and/or therapeutic vaccination against cancer may be used in low doses (when compared to antibodies against TAA for passive immunotherapy), typically less than 1 mg by injection. The antibodies also have a long continual activity that directly induces immunity and their shelf life is unlimited (fresh vaccination is always possible). This sequence represents the murine monoclonal antibody MAK HEZ variable region light chain fragment which is used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method of killing cancer cells, particularly prostate cancer cells, by directing a biological agent to
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   for
                                                                                                                                                to a
Novel use of antibodies against human cellular membrane antiqens
                                                                                                                                                                         human cellular membrane antigen, to manufacture a medicament to
prophylactically and/or therapeutically vaccinate against cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; antibody; heavy chain; prostate cancer; biological agent.
                                                                                                                                          This invention describes the novel use of an antibody targeted
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Pred. No. 1.2e-39;
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                                                                                Example 3; Page 47-48; 54pp;
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                              vaccination against cancer
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09-APR-1997;
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the cells which then binds to a prostate specific membrane antigen and causes the molecule to be internalised. The internalisation of the agent, which may be bound to a drug or which may act to kill the cell alone, then leads to the death of the cell. The present sequence forms part of an antibody which may be used as the biological agent of the invention. In addition to prostate cancer, the method can be used with renal, urothelial, colon, renal, lung and breast cancer cells, and cancerous cells of metastatic adenocarcinoma to the liver.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                               Chimeric; heavy chain; variable region; monoclonal antibody; lymphocyte function associated antigen-3; LFA-3; inflammation; autoimmune disease; immunomodulation; systemic lupus erythematosus;
                                                                                                                                                                                                                 1 NIVMIQSPKSMSMSVGERVILICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYIGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light and heavy chain variable region sequences were deduced from the DNA sequences obtd. by PCR of DNA sequences obtd. from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               auto:immune
                                                                                                                                                               Length 107;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                       61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                  Monoclonal antibodies active against lymphocyte function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tigen-3 - for treating influencion and for detecting LFA-3 protein in a sample
                                                                                                                                                          100.0%; Score 562; DB 22;
100.0%; Pred. No. 1.2e-39;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1E6 kappa light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
24..34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis; thyroiditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wallner BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 14; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                 AAR27144 standard; Protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92EP-0104318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910S-0667975
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                          Similarity 100.
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-309758/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOJ ) BIOGEN INC
                                                                                                                       107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chisholm PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1992
                                                                                                                                                                                       107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP503646-A.
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                                                                                                                       Sequence
                                                                                                                                                             Query Match
Best Local S:
Matches 107,
                                                                                                                                                                                                                                                                                                                                                                                            AAR27144;
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domain
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                                                                                                                                                                                                                                                                                               61
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ID AAR2
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hybridoma cell line lE6-2C12 (ATCC HB 10693). The light and heavy chain regions may be used to construct a monoclonal antibody active against LFA-3 which blocks adhesion of LFA-3 expressing cells to lymphocytes. The antibody may be used in the treatment and diagnosis of acute and chronic inflammation, autoimmune diseases and for immuno-modulation including systemic lupus erythematosus, rheumatoid arthritis and thyroiditis. See also AAR27145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; monoclonal antibody; J591; prostate specific membrane antigen; cancer; vascular endothelial cell; metastatic adenocarcinoma.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                         Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for
                                                                                                                                                                                                                                                                     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                    0
                                                                                                                                                                                              Length 109;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                          61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                            Score 562; DB 13;
Pred. No. 1.3e-39;
                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse J591 monoclonal antibody light chain.
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 12; Page 57; 94pp; English.
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                                                                                                                                                                                                                  Best_Local Similarity .vv. Matches 107; Conservative
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                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                 109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-1998
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                                                                                                                                                  Sequence
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AAW47085
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is used to treat renal, urothelial, colon, lung, rectal or breast cancers and metastatic adenocarcinoma of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cener (presence of PSMA in the serum indicates that prostate cells are being lysed). (A) binds to an epitope of PSMA expressed on live cells (contrast antibody 7E11 which only binds after cell lysis), allowing targeting of live, both cancer cells themselves and the VEC on which they depend are killed. All VEC close to cancer cells express PSMA, whatever the type of cancer, but normal VEC do not.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the kappa light chain of the monoclonal antibody J591. The invention relates to an isolated antibody or its antigen binding portion (I) which binds to an extracellular domain of prostate specific membrane antigen and which does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells. (I) is useful for diagnosis of diseases associated with the presence of normal, benign hyperplastic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody specific for extracellular prostate-specific membrane antigen, useful for diagnosis and treatment of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J591 monoclonal antibody; extracellular domain; diagnosis; therapy; prostate specific membrane antigen; prostate cancer; kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                 1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J591 monoclonal antibody kappa light chain protein sequence #1.
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                                                                                                                                                                                                                                                                                           Length 121;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           rttgsgsatdftltissvqaedladyhcgqgysypytfgggtkleik 113
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                       100.0%; Score 562; DB 19;
100.0%; Pred. No. 1.4e-39;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 12; Fig 10; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                     121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6107090-A.
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                                                                                                                                                                                                                                       Sequence
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the disease is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used alone or bound to a substance effective to kill cancerous prostate epithelial cells as a therapy for prostate cancer. Binding and internalising of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cytotoxic spense. (I) targets only prostate epithelial cells and other tissue are spared which provides safer treatment particularly for elderly patients. The antibodies bind to living prostate cells and treatment using these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating or killing cancerous, especially non-prostate, cells (e.g. breast cancerous cells or cancerous cells of metastatic adenocarcinoma to the
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                            1 NIVMTQSPKSMSWSGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                             Mouse; antibody; heavy chain; prostate cancer; biological agent.
                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                            Length 121;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                              61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine monoclonal antibody J591 kappa light chain #1.
                                                                                                                                                                                                                                                ; DB 21;
1.4e-39;
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                            100.0%; Score 562; 100.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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96US-0022125.
97US-0838682.
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                                                                                                                                                                                                                                                                           Matches 107, Conservative
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                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                               121 AA;
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09-APR-1997;
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                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    liver)
                                                                                                                                                                cells.
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invention. In addition to prostate cancer, the method can be used with
                                                                                                                                   Gaps
                                                                                                                                                                              useful in the treatment of myocardial infarction, cerebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, panorreattis, acute kidney failure, chronic rheumatism, cardiac shock, panorreattis, ault respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myelome 93U1 (93363Ag8 U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity.
                                                                                                                                                                1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
               renal, lung and breast cancer cells, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis; cerebral infarction; acute kidney failure; colitis; chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing; disease; hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody inhibiting type II phospholipase A2 activity for treatment of myocardial and cerebral infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibodies which inhibit type II phospholipase A2 are
                                                                                                                                                                                                                                                                                                                                                                                                                           MAb 10.1 light chain, directed against type II phospholipase A2.
                                                                                                                                   ·.
                                                                                                     Length 121;
               renal, urothelial, colon, renal, lung and breast cancer ce
cancerous cells of metastatic adenocarcinoma to the liver
                                                                                                                                   Indels
                                                                                                                                                                                                                         100.0%; Score 562; DB 22;
100.0%; Pred. No. 1.4e-39;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                   AAW01145 standard; Protein; 127
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/label= CDR
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/label= CDR
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/label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1996-333946/33
                                                          121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT40805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding-site
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                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                  AAW01145;
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Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture supernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CL4B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly suitable for preclinical testing.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                   1 nivmtqspksmsmsvgervtltckasenvvtyvswyqqkpeqspklliygasnrytgypd 80
                                                                                                                                                                                                     NIVMTQSPKSMSNGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancers, esp. Hodgkinson's disease.
Cytoplasmic RNA was isolated from cells of the mouse myeloma hybrid line Ber-H2. cDNA was isolated using reverse transcriptase. A WIDJ fragment contg. band was cut from a gel and purified. DNA corresponding to VK and Vgamma was isolated and cloned into vectors. Oligonucleotides used are given in AAT58331 to AAT58340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The ligands are useful for diagnosis or therapy of CD30 expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA mols. encoding CD30-specific immunoglobulin variable regions
                                                                                                                                                                         ;
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                                                                                                                                             Length 127;
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                           Score 562; DB 17;
Pred. No. 1.5e-39;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for cancer diagnosis or therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1.29
30.136
/label= mat_protein
                                                                                                                                                                                                                                                                                                                                                           AAW01632 standard; Protein; 136 AA
                                                                                                                                             100.0%; Sc
100.0%; Pr
live 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 15; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95DE-1043039
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ber-H2 heavy kappa chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; Ber-H2
                                                                                                      127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21..127
/note= "Mature mouse antibody AF2 light chain variable
                                                               Gaps
                                                   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-interferon for the treatment of autoimmune diseases, e.g. multiple sclerosis and diabetes -
                          .;
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Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109..117
/label= CDR
/note= "Complementarity determining region"
                           Indels
                                                                                                                  61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                   Mouse AF2 antibody light chain variable region (AF2-VL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determining
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 Score 527; DB 17;
Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-terminal peptide"
                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70..76
/label= CDR
/note= "Complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vasquez M, Landolfi NF, Tsurushita N,
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region (AF2-VL)"
                          5;
                                                                                                                                                                                           AAY71545 standard; Protein; 127
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  3.88;
Similarity '94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14..54
/label= CDR
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                            Conservative
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N-PSDB; AAD01345.
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                 Best Local Sim
Matches 101;
                                                                                                                                                                                                                    AAY71545;
   Query Match
Best Local
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AAW00828;
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                                                                                                                              versus host disease following organ transplant, Type I diabetes, multiple sclerosis, rheumatoid arthritis, psoriasis, systemic lupus erythematosus (SLE), Hashimoto's thyroiditis, primary biliary cirrhosis and inflammatory bowel disease like, Crohn's disease.
The present amino acid sequence is the mouse AF2 antibody, light chain variable region (AF2 vL). It has IgG2b isotype and kappa light chain. It is used for the construction of humanised version of mouse AF2 antibody HuZAF, that comprises mouse antibody AF2 complementarity determining regions (CDRs), functionally joined to the human acceptor antibody EU framework region (FR). HuZAF antibody specifically binds to and neutralises gamma-interferon (IFN). They can also block the binding of mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences that are immunogenically active in humans and remains unaffected by immune responses, that may reduce its activity or circulating half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell-
                                                                                                                                                                                                                        Score 521; DB 21; Length 127; Pred. No. 3.6e-36;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                   RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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4
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                                                                                                                                                                                                                                               5; Mismatches
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                                                                                                                                                                                                                        92.78;
91.68;
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89US-0310252.
90US-0590274.
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                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                      Sequence 127 AA;
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Best Local Simi
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13-FEB-1989;
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                                                                                                                                                                                                                        Query Match
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                       immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft versus. Host diseases, transplant rejection, autoimune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody specifically recognising the Fas ligand - useful for the detection of Fas ligands either on cell surface or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the light chain variable region of the anti-human Fas ligand monoclonal antibody (MAD) NOK-3. NOK-3. is produced by the hybridoma NOK-3 (FERM BP-5046), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x65Ag8-653 (AFCC CRL-1580) cells. The MAD recognises the human Fas ligand on the cell surface or in solution, and can be used to
                                                                                                                                                                                                                                                        and myeloid leukaemia. The present sequence is an antibody used to demonstrate the method of the invention.
present invention describes a method of producing humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable region; light chain; human; Fas ligand; monoclonal; antibody; NoK-3; hybridoma; inhibition; apoptosis; assay; diagnosis; disease; hepatitis; infectious mononucleosis; systemic lupus erythematosus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
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Pred. No. 3.9e-36;
5; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.7%;
Best Local Similarity 91.6%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                           136 AA;
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W09717446-A2
         09-JUN-1994;
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                       09-JUN-1993;
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                                                                                    Gaps
                                                                                                 inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay in biological samples (e.g. human blood), especially for disease diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
                                                                                                                                                                                                                                                                                                                                                                                                   Vlabel Linker
Mootes "linker connecting the VH and VL regions"
135..239
                                                                                   0;
                                                                                                                                                                                                                                                                                                                                               'note= "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                            "complementarity determining region 3"
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/note=_"complementarity determining region 3"
                                                                   90.6%; Score 509; DB 17; Length 108; 90.7%; Pred. No. 3e-35; tive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label = CDRI
/note = "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining region
                                                                                                                                                                                                                                               SCFV; single chain Fv; HCG; human chorionic gonatotropin; Aspergillus; Mucor; Neurospora; Penicillium; pUR4138; monoclonal antibody; Clearblue; fusion protein;
                                                                                                                                      RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                         "MAb Clearblue VH region
                                                                                                                                                                                                                                                                                                                                                                                                                          .35..239
|Tabel= VL
|note= "MAb Clearblue VL
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                    A.
                                                                                                                                                                                    AAR64812 standard; Protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Myc_tail
                                                                                                                                                                                                                                                                                                                                                                                    /label= CDRIII
                                                                                                                                                                                                                                                                                                                                                       47..63
/label= CDRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDRII
                                                                                                                                                                                                                                                                                                                                        /label= CDRI
                                                                                                                                                                                                                                                                                                                  /label- VH
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                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                      antibody engineering.
                                                                          Local Similarity
es 97; Conserva
                              lupus erythematosus
                                              108 AA;
                                                                                                                                                                                                                                ScFv anti-HCG
                                                                                                                                                                                                                 15-JUL-1995
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Best Local Si
Matches 97;
                                               Seguence
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Variable light sequence; murine antibody 24-31; gp39; humoral immunity; activated CD4+ T cell, sell proliferation; immunodeficiency disease; human V-Kappa subgroup I; DEN; germline 012; rheumatoid arthritis; multiple sclerosis; diabetes; systemic lupus erythematosus; ITP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable light subunit variant 4 of humanised murine antibody 24-31.
                                                                                                                                                                                                                                                                                                                                                                Prodn. of single chain Fv antibody fragments - as fusion proteins using a transformed mould of the genus Aspergillus, Mucor,
                                                                                                                                                                                                                                                     Van Den Hondel CAMJJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The PstI-XhoI fragment (given in AAQ76275) of pUR4138 encode the ScFv fragment (AAR64812) of anti-HCG monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 239;
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85.7%; Pred. No. 1.1e-32;
tive 10; Mismatches 5;
                                                                                                                                                                                                                               essing JGM, Musters W;
Verbakel JMA, Verrips CT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 13-14; 70pp; English.
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                                          93EP-0201660.
93EP-0201661.
93EP-0201706.
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94WO-EP01906
                                                                                                                                                                                                                                  Hessing JGM,
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                                                                                                                                       NEDE ) NEDERLAND ORG TNO.
                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora or Penicillium
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                                                                                                                                                             (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
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Best Local Similarity
Matches 90; Conserv
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WPI; 1997-281035/25.

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The present sequence represents a humanised variable light sequence of murine antibody 24-31, and is a variant of AAW21933 Antibody 24-31 binds to gp39, a type II human membrane protein, which has a novel role in the regulation of humoral immunity. The gp39 protein is expressed on activated CD4+ T cells. Cells possessing the gp39 protein on their surface can trigger a B cell proliferation, and thus induce antibody production. Several immunodeficiency diseases are caused by mutant gp39 protein. Murine antibody variable light sequence was humanised using as templates the human V-Kappas subgroup I DNA sequences e.g. LEN, as wells as germline 012. DNA encoding the present sequence is used to create a humanised antibody for inhibiting CD40 binding to gp39. The humanised antibody for inhibiting CD40 binding to gp39. The humanised antibody is less immunogenic than the non-humanised murine version, and therefore does not result in a neutralising antibody response, which is problematic if the antibody is to be administered repeatedly. The humanised antibody can be used to treat a disease treatable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulating gp39 expression or inhibiting the gp39/Cd40 interaction, specifically an autoimmune disorder (e.g. rheumatoid arthritic, portrasis, multiple sclerosis, diabetes, systemic lupus erythematosus and ITP), or non-autoimmune disorder (e.g. graft versus host disease or graft rejection).
                                                       Humanised antibody capable of competing with, or derived from, murine 24 - 31 antibody – useful to modulate gp39 expression or inhibiting gp39/CD40 interaction
                                                                                                                                                                             Claim 7; Page 75; 106pp; English.
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0; Gaps 1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60 80.8%; Score 454; DB 18; Length 107; 80.4%; Pred. No. 1e-30; tive 10; Mismatches 11; Indels (Query Match 80.8 Best Local Similarity 80.4 Matches 86; Conservative

107 AA;

Sednence

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Op

61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

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Search completed: December 27, 2001, 09:01:01 Job time: 57 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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using sw model protein search, OM protein December 27, 2001, 09:01:39 ; Search time 25.84 Seconds (without alignments) 315.429 Million cell updates/sec Run on:

US-09-889-300A-2 562

1 NIVMTQSPKSMSMSVGERVT......CGQGYSYPYTFGGGTKLEIK 107 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	Descrip		Id kappa chain	Iq kappa cha	Iq kappa cha	Ig light chain	Ig kappa cha	PI	PI	ant		Iq	pI	KVMS11 Ig kappa chain pr	Ig kappa chain	Ig kappa chain	gI	Ig	Į I	Ig k	anti-idio	Ig kappa	pI	307 Ig	264 Ig	184 Iq	PI 651	3285 Iq	0538 I	0000
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	Score	562	551	515	498	464	459	454	446.5	440	432	429	427	422	419	416	410	410	409	407	407	404	403	403	7	398.5	396	395	395	100
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Ouery Match 100.0%; Score 562; DB 1; Length 136; Best Local Similarity 100.0%; Pred. No. 2.2e-42; Matches 107; Conservative 0; Mismatches 0; Indels

Ig kappa chain V r PL7-6 antbody lig Ig light chain V r Ig kappa chain V r	SLN	nn 02-Apr-1982 #text_change 22-Jun-1999 ' A01917 C. Inoglobulin mRNA using specific priming and the d 9477 ding protein. 2051 ith conceptual translation 52098; PIDN:AAC37684.1; PID:9452099 tramer subunit consists of two identical light (such as 1gA and 1gM, the subunits associate into bulin s predicted <sig> gion (MOPC 21) #status experimental <mat> ogy <imm></imm></mat></sig>
B28195 526336 122270 526336 138601 PD0263 PC1083 PC	ALIGNMENT	BEULT 1 WES21 9 Kappa chain precursor V region (MOPC 21) - mo :Species muse musc clus of house mouse) Accession: A93736; A90262; B49982; A01917 Hamlyn, P. H.; Gait, M.J.; Milstein, C. Title: Complete sequence of an immunoglobulin Reference number: A93736; MUD: 82059477 Tatle: Complete sequence of an immunoglobulin Reference number: A93736; MUD: 82059477 Wolecule type: mRNA Residues: 1.128 (427-444, 1972 Title: The complete amino acid sequence of a mino acid sequence in the sequence in the sequence of a mino acid sequence in the concept section acid sequence acid
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7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		main precursor v Mus musculus (ho Mus musculus (ho Mus musculus (ho Mus musculus) (ds 193736; 490262) (ds 193736; 493736; (r) Mustein, C. (r)
E E E E E E E E E E E E E E E E E E E		KESULT 1 KVMS21 Ig kappa chain precursor V C:Species Mus musculus (ho C:Species
0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		KESULT 1 KVMS.1 Ig kappa chain precursor V region (MOPC. Species: Mus musculus (house mouse) C. Species musculus musculus (house mouse) C. Caccession: A93736; A90262; B49982; A011 C. Accession: A93736; A90262; B49982; A011 C. Accession: A93736; A485-4494, 1981 A.Title: Complete sequence of an immunog A; Reference number: A93736; MUD: 8205947 C. Biochem. J. 128 (427-444, 1972 A; Residues: 1-136 (4MA) R; Svasti, J.; Milstein, C. Biochem. J. 128 (427-444, 1972 A; Residues: 1-136 (4MA) A; Residues: Boorgel emino acid sequence A; Reference number: A90262; MUD: 305331 CA; Residues: 30-136 (5VA) A; Residues: 30-136 (5VA) A; Residues: 30-136 (5VA) A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; MUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A; Accession: B49982 A; Reference number: A9982; NUD: 9413205; A;
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R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S. Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated ger A;Reference number: A33932; MUID:8928283
A;Accession: I33932
A;Accession: I33932
A;Accession: I3992
A;Molecule type: mRNA
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A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
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A;Residues: 1-107 <CIM>
A;Cross-references: EMBL:X76019; NID:9416090; PIDN:CAA53606.1; PID:91333952
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000 C;Accession: PL0268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig light chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                  A; Residues: 1-118 <BAC>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 39-113/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118
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88.8%; Pred. No. 1.5e-36;
iive 6; Mismatches 6;
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Pred. No. 7.5e-37;
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submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Accession: S38713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYP 95
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Mismatches
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A;Accession: PL0268
                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 100.0%; P. Conservative 0;
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Best Local Similarity 88.8
Matches 95; Conservative
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Best Local Similarity
Matches 95; Conserv
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C; Accession: I33932
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R:Tempest, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Mard
submitted to the EMBL Data Library, May 1993
A; Description: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act
A; Reference number: S33131
                                                                                                                                                                                                                                                                                                                                 antibody properties of anti
                                                                                                                                         Ig kappa chain V region (129) - mouse

C; Species: Mus musculus (house mouse)

C; Accession: D37266

R; Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A; Title: Heavy and light chain variable region sequences and antibody properties A; Reference number: A38740; MUID: 91177923

A; Accession: D37266

A; Status: preliminary; not compared with conceptual translation

A; Residues: 1-111 < RUFA

A; Residues: 1-111 < RUFA

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 19-93/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb_1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA .

A; Residues: 1-107 «TEXP>
A; Residues: 1-107 «TEXP>
A; Cross-references: EMBL:222670; NID:9297473; PIDN:CAA80379.1; PID:9297474
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 DIVMIQIPKSMSMSWGERVTLTCKASENVVIYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Query Match 98.0%; Score 551; DB 2; Best Local Similarity 98.1%; Pred. No. 1.7e-41; Matches 105; Conservative 1; Mismatches 1.

64

음 δ Q Query Match 91.6%; Score 515; DB 2; Le Best Local Similarity 92.5%; Pred. No. 2.2e-38; Matches 99; Conservative 3; Mismatches 5;

A; Accession: S33132 A; Status: preliminary

precursor V region (E7) - mouse

Ig kappa chain

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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0204
R;Smith, R.G; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies fro A;Reference number: PL0198; MUID:90309768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb_1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X70097; NID:g288262; PIDN:CAA49701.1; PID:g288263 Cs. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer: immunoglobulin homology < IMS-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                    1 SPKSMSMSVGERVTLSCKASENVGTYVSWYQQKP-QSPQLLIYGASNRYTGVPDRFTGSG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-108 <SMI>
A; Cross-references: GB:X53644; NID:950198; PIDN:CAA37695.1; PID:9930144
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.48; Score 446.5; DB 2;
93.58; Pred. No. 1.8e-32;
... utematches 2;
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Pred. No. 3.9e-31;
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A:Reference number: S32185
A:Accession: S32192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;24-34/Region: complementarity-determining 1
F;50-56/Region: complementarity-determining 2
F;96-108/Region: complementarity-determining 3
F;96-108/Region: JH region
                                                                                                                                                                                                                                                                                                                                 86
        C;Keywords: immunoglobulin
F;10-83/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                       91
                                                                                                                                                                                                                                                                                                                                 67 SATDFTLTISSVQAEDLADYHCGQGYSYPYTF
                                                                                                                                                                                                                                                                                                                                                             76.98;
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Conservative
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Best Local Similarity
                                                                                                              Query Match
Best Local Similarity
Matches 86; Conserv
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A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
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R; Izui, S.
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgW and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444
A;Accession: PH1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ignight chain V region (clone 165.3m) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1071
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444
A;Accession: PH1071
A;Status: nucleic acid sequence not shown
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C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NIVMAMSPKSMSMSVGERVTLSCKASENVGTYVSWYQQTPEQSPTLLIYRASDRYFGVPD 60
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                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 459; DB 2;
Pred. No. 1.7e-33;
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1larity 93.9%; Pred. No. 4.2e-33;
Conservative 1; Mismatches 3.
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A;Residues: 1-91 <TLL>
A;Experimental source: B cell, strain [NZB x NZW]F1
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C; Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;4-34/Region: complementarity-determining 1
F;50-56/Region: framework 2
F;50-56/Region: framework 3
F;57-88/Region: framework 3
F;99-97/Region: framework 3
F;98-97/Region: framework 4
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                                                                                                                                                                                                                                                                                                    81.7%;
82.2%;
                                                                                                                                                                                                                                                                                                                              Local Similarity 82.2
hes 88; Conservative
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Best Local Similarity
Matches 92; Conserv
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A;Cross-references: EMBL:X14622; NID:952400; PIDN:CAA32775.1; PID:952401
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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ilarity 78.5%; Pred. No. 4e-3
Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64-129/Disulfide bonds: #status predicted
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A; Residues: 41-149 <RAB>
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Best Local Similarity
Matches 84; Conserv
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A; Residues: 1-127 <KOF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Smith, G.P.
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                                                   RESULT
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C.Species: Mus musculus (house mouse)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C.Accession: $42466
R.Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
Submitted to the EMBL Data Library, March 1994
A.Reference number: $42466
A.Reference number: $42466
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-117 < SHL>
A.Gross-references: EMBL.X78108; NID:9460824; PIDN:CAA54998.1; PID:9460825
C.Superfamily: immunoglobulin V region: immunoglobulin homology
C.Reywords: heterotetramer: immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32191
R;Izul, S.
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Gaps
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                                                                                                1 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPD 60
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14; Indels
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8; Mismatches
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nes 84; Conservative
85; Conservative
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-107 <IZU>
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RESULT

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A; Molecule type: protein
A; Residues: 30-149 SMI>
A; Residues: 30-149 SMI>
A; Residues: 30-149 SMI>
A; Residues: 30-149 SMI>
A; Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not the object of the amino end, due to a tan 42 corresponds to the amino-terminal residue of typical kappa chains.
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds: In some cases, such as 19A and 19M, the subunits associate into C; Reywords: duplication; heterotetramer; immunoglobulin homology
C; Reywords: duplication; heterotetramer; immunoglobulin homology
F; 30-149/Product: Ig kappa chain V region (MPCII) #status experimental CMAT>
F; 57-131/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S0457
R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.
R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.
A;Description: Complexity, polymorphism and connectivity of murine V(kappa) gene fami
Ig Kappa chain precursor V region (MPC11) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 1984 *Requence_revision 19-Feb-1984 *text_change 21-Jan-2000 C;Accession: A90823; A90733; A90798; A01916 R;Kelley, D.E.; Coleclough, C.; Perry, R.P. Celley, 581-689; 1982 A;A;tle: Functional significance and evolutionary development of the 5'-terminal region A;Reference number: A90823; MUID:83001944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. 171, 337-347, 1978
A;Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC A;Reference number: A90298; MUID:78186617
A;Contents: myeloma protein MPC11
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A;Residues: 1-71 <KEL>
A;Note: the sequence was determined from the differentiated
A;Note: T.H.; Hulyn, P.H.; Matthyssens, G.; Roe, B.A.
R;Rabitts, T.H.; Halyn, P.H.; Matthyssens, G.; Roe, B.A.
Ra;Rabitts, T.H.; alforem. 58, 176-187, 1980
A;Title: The variability, arrangement, and rearrangement of
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RESULT 15
P00265
Ig kappa chain V region (MC1) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1992 #text_change 21-Jan-2000
C; Accession: P00265
R; Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A; Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal A; Reference number: P00265
A; Tette: Sequence analysis of the variable region of a mouse gene encoding a monoclonal A; Reference number: P00265
A; Recession: Complementarity-determining 1
F; 82-08/Region: complementarity-determining 2
F; 101-109/Region: complementarity-determining 3
F; 101-109/Region: complementarity-determining 3
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F;1-20/Domain: signal sequence #status predicted <SIG> F;21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT> F;36-110/Domain: immunoglobulin homology <IMM>
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74.0%; Score 416; DB 2;
Best Local Similarity 77.6%; Pred. No. 1.1e-29;
Matches 83; Conservative 8; Mismatches 16
                                                                                                                                         Query Match 74.6%; Score 419; DB 2; Best Local Similarity 75.7%; Pred. No. 6.3e-30; Matches 81; Conservative 10; Mismatches 16
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US-08-452-164A-55
US-08-976-183A-36
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US-08-926-591-16
US-08-224-591-18
US-08-226-789-18
US-08-926-789-18
US-08-926-789-18
US-08-653-402B-4
US-08-653-402B-4
US-08-6133-804-2
US-08-461-184-8
US-08-461-1386-2
US-08-461-1386-2
US-08-461-1386-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1172
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 107 amino acids
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Best Local Similarity
       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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       RESULT
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(without alignments)
106.213 Million cell updates/sec
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Sequence 1, Appli
Sequence 103, App
Sequence 103, App
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-US92-02044-2
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Maximum DB seq length: 2000000000
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Sequence 16, Application US/08838682
Patent No. 6107090
GENERAL INFORMATION:
APPLICANT: QANGEL M.D. Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE TITLE OF INVENTION: CANCER NUMBER OF SCOURCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: (US/UB/7838,682)
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STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
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Pred. No. 1.7e-50;
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REFERENCE/DOCKET NUMBER: B150CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jr., James F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 107; Conservative
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STATE: New York
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US-09-357-710A-16
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Patent No. 6136311
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
APPLICANT: BANDER: Neil H.
NUMBER OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
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100.0%; Pred. No. 1.7e-50;
iive 0; Mismatches 0;
0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAX-1996
PRIOR APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-UUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,682
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERNCE/DOCKET NUMBER: 19603/1173
TELECOMMUNICATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 107; Conservative
Matches 107; Conservative
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                                                GENERAL INFORMATION:

APPLICANT: Bander, Neil H.

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025

CURRENT APPLICATION NUMBER: US/09/357,710A

CURRENT APPLICATION NUMBER: US 08/838,682

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR PLILING DATE: 1996-05-06

PRIOR FILING DATE: 1996-05-06

PRIOR FILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.0
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APPLICANT: SANO VICEL L.
APPLICANT: CHISHOFM PARTICIA L.
APPLICANT: WALLNER, Barbara P.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING
TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No. 1.7e-50;
iive 0; Mismatches 0;
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APPLICATION NUMBER: PCT/US92/02044
FILING DATE: 19920312***
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,975
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PCT-US92-02044-2
; Sequence 2, Application PC/TUS9202044
; GENERAL INFORMATION:
Sequence 16, Application US/09357710A Patent No. 6290956
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TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 121 amino acids
amino acid
                                     al Similarity 100.
107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: U.S.A.
14603-1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                              RESULT 6
US-08-895-914-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: 1
STATE:
                      Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                         1 NIVMIQSPKSMSMSWGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                        Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08838682
Patent No. 6107090
GENERAL INFORMATION:
APPLICANT: (Bander M.D., Neil H.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        Query Match
100.0%; Score 562; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.7e-50;
Matches 107; Conservative 0; Mismatches 0;
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30,727
38: 19603/1172
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: (US/08/838, 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19 TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
              TELEFAX: (212) 715-0600
TELEAX: (212) 715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 11
                                                                                                                : 109 amino acids
AMINO ACID
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amino acid
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PCT-US92-02044-2
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MOLECULE TYPE: protein
US-08-838-682-11
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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: U.S.A.
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                                                Gaps
                                                                                                                  7 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66
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  Length 121;
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                                              Indels
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                                                                                                                                                                                                           61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: (Bangler, Neil H.
TITLE OF INVENTION: TREATMENT AND DIACNOSIS OF CANCER
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
100.0%; Score 562; DB 3; 100.0%; Pred. No. 1.9e-50;
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1173
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA: BAPLICATION NUMBER: US 08/838,682
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08895914 Patent No. 6136311
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IBM PC compatible
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FILING DATE: 28-SEP-1990
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Bander, Neil H.

TITLE OF INVENTION:

FILE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/357,710A

CURRENT APPLICATION NUMBER: US/09/357,710A

CURRENT FILING DATE: 1999-07-20

PRIOR PEPLICATION NUMBER: US 60/016,976

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1996-05-06

PRIOR PELING DATE: 1996-05-06

PRIOR PELING DATE: 1996-05-06

PRIOR PELING DATE: 1996-05-06

PRIOR PELING DATE: 1996-05-06

PRIOR FILING DATE: 1996-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 121;
67 RFTGSGSATDFTLTISSVQAEDLADYHCGGGYSYPYTFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, Wicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, HAROWED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.25
STRENT APPLICATION DATA:
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100.0%; Pred. No. 1.9e-50;
iive 0; Mismatches 0;
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19-DEC-1990
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                                                                                                                                      Sequence 11, Application US/09357710A
Patent No. 6290956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application \text{US}/\text{O7634278} Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-11
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LENGTH: 121
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INFORTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 521; DB 1;
Pred. No. 3.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
92.7%; Score 521; DB
Best Local Similarity 91.6%; Pred. No. 3.3e
Matches 98; Conservative 5; Mismatches
                                     APPLICATION NUMBER: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 128-DEC-1988
ATTOKNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-0026
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 326-2400
TELEFRX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
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APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
FILLING APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
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FILING DATE: 13-FEB-1989
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application US/08477728 Patent No. 5585089
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, HATOLG E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     92.7%; Score 521; DB 1; 91.6%; Pred. No. 3.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
        REFERENCE/DOCKET NUMBER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
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FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 99, Application US/08487200 Patent No. 5693762
                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ 1D NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 326-2400
                                                                                                                              LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                           98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO, Man Sung
                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-474-040-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 28-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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California
                                                                                                                                                                        linear
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GENERAL INFORMATION:
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                                                                                                                                                                      TOPOLOGY:
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US-08-487-200-99
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
                                                                                                                                                                                                                                                                                                                                                    Score 521; DB 1;
Pred. No. 3.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                            REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFA: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/590,274
FILIND DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILIND DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 99, Application US/08474040; Patent No. 5693761; GENERAL INFORMATION:
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INPORMATION:
NAME: Smith, William
NEGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                    92.7%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 379 Lytton Avenue CITY: Palo Alto
STATE: California
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APPLICATION NUMBER: US 07
FILING DATE: 19-DEC-1990
                                                                                                                                                                                                        : 136 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-477-728-99
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                    linear
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Best Local Similarity
Matches 98; Conserv
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GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabila
APPLICANT: HANNA, Nabila
APPLICANT: PADLAN, Eduardo A.
APPLICANT: PEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                         Gaps
                                                                                                                                                                                                             1 NIVMIQSPKSMSMSVGERVTLICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
                                                                                                                                                                                                                                  30 NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
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                                                                                                                            Score 521; DB 4; Length 136; Pred. No. 3.3e-46;
                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                    90 RFTGSGSATDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136
                                                                                                                                                                                                                                                                                              61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTE: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.8%; Score 454; DB 3;
80.4%; Pred. No. 1.7e-39;
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                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
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07-NOV-1995
NN: 536
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                            92.7%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 107 amino acids TYPE: amino acid
                                                                                                             Query Match
Best Local Similarity 91.6*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. Box 1404
                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-484-537-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria STATE: Virginia
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US-08-554-840-4
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Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS:
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                   90 RFTGSGSATDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                             Score 521; DB 1;
Pred. No. 3.3e-46;
                                                                                                                                                                                                                                                      5; Mismatches
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FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 07/310,252
13-FEB-1989
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith, William M
REGISTRATION NUMBER: 30.223
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
                         99
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                             Query Match 92.7%;
Best Local Similarity 91.6%;
Matches 98; Conservative
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TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-200-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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STATE: California
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Matches
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APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: PARMAN, Eduardo A.
APPLICANT: PEWMAN, FOLAND A.
APPLICANT: NEWMAN, FOLAND A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9p39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PADLAN, Eduardo A.
NEWMAN, Roland A.
VENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
VENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
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61 RFSGSGSGTDFTLTISSLQAEDVADYFCQQYNSYPYTFGGGTKLEIK 107
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNET AGENT INFORMATION:
NAME: Teskin, Robin L.
RECISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECHONE: (703) 836-620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                             Sequence 2, Application US/08554840 Patent No. 6001358 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-554-840-3; Sequence 3, Application US/08554840; Patent No. 6001358
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: United States
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APPLICANT: NEWMAN, F
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
STATE: Virginia
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STRANDEDNESS: sir
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APPLICANT: BLACK,
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                                                                                                           US-08-554-840-2
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                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/554,840 FILING DATE: 07-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.5%; Score 447; DB 3; Best Local Similarity 79.4%; Pred. No. 8.8e-39; Matches 85; Conservative 9; Mismatches 13
                 ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: December 27, 2001, 09:03:07 Job time: 183 sec
                                                                                                                                                                                                                                                                                                                                                                                                          012712-127
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERRICE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                 ADDRLC, P.C. SYREET: P.C. CITY: Alexandria STATE: Virginia STATE: Virginia COUNTRY: United States "TP: 22313-1404 "TP: ADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-554-840-3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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